79	6	26 212	46	66 332	392	106 452	126 512	146 572
GGACGGCTCCCGGCTGCAGTCTGCCCGCCCCCCCCCGCGGGGGGCCGAGTC	A GCG	C TGC	C TGT	CII	Y TAC	N AAT	, p	Q CAG
3666	P CCT	H CAT	C TGC	F TTC	M ATG	P CCA	P CCG	CCC
36660	Q CAG	K AAG	D GAC	W TGG	R CGC	P	GGA	S TCA
36060	RGGC	K AAA	E GAG	F	R AGG	Q CAG	G GGA	N AAC
3000	R AGG	A GCC	Y TAC	Y TAC	R CGG	R AGG	P CCA	CCC
၁၁၁၁	M ATG	E GAA	S	W TGG	I ATC	T ACC	D GAC	PCCA
ပညညာ	AGCC	T ACA	R CGC	L CTG	F TTC	Y TAC	T ACT	V GTC
STCTO	GCGCGCTGGAGGACGCGAGGAGCC	C TGC	C TGC	R AGG	F	S TCC	Y TAC	Q CAG
rgcac)CCC	E GAG	I ATA	Q CAG	9 9 9 9	V GTG	Y TAT	F TTC
GGGC	3AGG1	Γ	YTAT	I ATA	A GCC	N AAT	Р ССС	A GCT
CICC	rgga(L CTC	Y TAT	S TCC	G GGA	F TTC	P CCG	M ATG
4CGG	30801	L CTG	T ACC	L	C	A GCC	ე ეეე	A GCA
	36600	G GGG	P CCA	A GCC	C	P CCA	P CCG	M ATG
3CGT(TCCC	CIC	Y TAT	CGG GG	FTTC	E GAG	Q CAG	S TCC
3GAC(3660	L CTG	L	V GTG	L	E GAG	Q CAG	N AAT
CGCC	BACC	L CTG	G GGA	CTGT	V GTG	I ATC	A GCC	G GGG
3CGT(TGC	A GCG	E GAA	C	9 9 0	L CTG	GGA	V GTC
CCAC	၁၁၅၁၅	A GCG	FTTC	R AGG	M ATG	PCCG	P CCA	P
GTCGACCCACGCGTCCGCGGACGCGTGG	GCGAAGCGCCCTGCGACCCGGCGTCCGG	V GTG	Y TAT	S TCC	M ATG	P CCG	9 9	N AAC
GT(<i>1</i> 525	K AAG	W TGG	9 9 9	L	P CCC	P CCC	M ATG

Fig. 1A

BEST AVAILABLE CC.

166	632	173	653
ĿĴ	GAA		
X	TAC		
Ы	CCG		
Ы	CCC		
Ы	CCG		
Ы	CCT		
Ħ	ACG		
Z	AAC		
ن ت	TGC		
X	TAC		
Ø	225		
Ч	CCA		
Д	CCI		
Ъ	\mathcal{CCC}	*	TAG
Ъ	500	凶	AAG
ن ت	IGC	A K	225
A	CCC	V K	GTG AAG
>	GGG AGT GTG GCC TGC	>	
ഗ	AGT	>	GTA
ტ	999	Ø	CAG

1206 1996 696 1285 1443 1680 890 1048 1127 1364 1522 1601 1759 1838 1917 IGIGIGAACGCIGACCIGICCIGICCIAAGAGCIAIGCAGCITAGCIGAGCCCCAAGAITACTAGAIGIGCIGIAI CACGGGGAATGAGGTGGGGGGTGCTTATTTTAATGAACTAATCAGAGCCTCTTGAGAAATTGTTACTCATTGAACTGG AGCATCAAGACATCTCATGGAAGTGGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG TGGGGTGCCCACGTGCAAGAGAGAGAGAGAGAGAGGGCCTTTCCCTGGCCTTTCTGTTCGTTGATGTTCACTTCCAG TGCTGGAGGTGCAGGTGGCATGTAGAGGGGCCAGGCCGAGCATCCCAGGCAAGCATCCTTCTGCCGGGTATTAATAGG CTGTTCATATCCTAAAGATAGACTTCTCCTGCACCGCCAGGGAAGGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGC CTICCIGCCCCAAACIGAGACATIGCATITIGIGAGCICTIGGICTGATITGGAGAAAGGACIGITACCCATITITIG CICTCCAGGGCATICICAGGCCCGGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGGTTCTGAAGGGTGCTTTCAAA TGCACTGACCATGTTGTCATAATTAGAATAAAGAAGTGGTCGGAAATGCACATTCCTGGATAGGAATCACAGCTCA CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGGGGCTAGTTCCGCCGCATAGTTATAGTGTTGA <u> AGTACAATATATGAACTCACACTTTGTCTCCTCTGTTGCTTCTGTTTCTGACGCAGTCTGTGCTCTCACATGGTAGTGT</u>

2470 2865 2549 2628 2707 AACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAAACAGACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG CCACCAGIGICICIGACCACCCIGGIGIGACIGCIGACIGCCAGCGIGGIACCICCCAIGCIGCAGGCCICCAICIAAA TGAGACAACAAGCACAATGTTCACTGTTTACAACCAAGACAACTGCGTGGGTCCAAACACTCCTCTTCCTCCAGGTCA TITGITITGCATITITAATGICITIATITITGIAATGAAAAAGCACACIAAGCIGCCCCTGGAATCGGGTGCAGCTGA TIGIGCCCACTICCIGGAGIGAGACAGCICCIGGIGIGIAGAAIICCCGGAGCGICCGIGGIICAGAGIAAACIIGAAG ATAGGCACCCAAAAGTCCGTGACTAAATTTCGTTTGTCTTTTTGATAGCAAATTATGTTAAGAGACAGTGATGGCTAGG CAGATCTGTGCATGCTTTTCCTCTGCAACAATTGGCTCGTTTCTCTTTTTTTGTTCTCTTTTTGATAGGATCCTGTTTCCT AAAAAAAAAGGGGGGCGGCCGC

Fig. 1C

GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCCTCGCTGGAGCC ATG GGC CGC CGG CTC

G R V A A L L L G L L V E C T E A K K H GGC AGG GTG GCG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT

Fig. 1D

DOZESEL DILGOL

45	65 331	85 391	105 451	125 511	145 571	165 631	173 655
C	F TTC	M ATG	P CCA	PCCC	P CCT	YTAT	
D GAC	W TGG	R CGC	P CCA	G GGA	S TCA	PCCC	
E GAA	F TTT	R CGG	Q CAG	G GGA	N AAT	P	
Y TAT	$_{\rm TAT}^{\rm Y}$	R CGC	R AGG	PCCT	P CCC	P CCA	
S TCC	W TGG	I ATT	T ACC	D GAC	Q CAG	P CCT	
R CGT	L CIG	F TTC	Y TAT	T ACC	V GTC	T ACG	
C HGC	R AGG	F TTC	S TCC	Y TAC	Q CAG	N AAC	
I ATA	Q CAG	G GGT	V GTG	Y TAT	F	C II GC	
Y TAT	I ATA	A GCC	N AAT	P CCA	A GCT	Y TAC	
Y TAC	S TCC	G	F TTC	P	M ATG	S	
T ACA	L	C TGT	T ACA	G GGA	A GCT	P CCT	
P	A GCC	C TGC	P	M ATG	M ATG	P CCT	
Y TAT	R AGG	${ m F}$	E GAG	Q CAA	T ACC	PCCC	* TAG
L	V GTG	L CTG	E GAG	Q CAG	N AAT	P CCA	K AAG
GGA	C TGT	V GTG	I ATT	A GCA		Y TAC	D GAC
E GAA	C H@C	G GGT	L	G GGA	V GTT	T ACT	K AAG
F TTT	R AGG	M ATG	P CCA	P CCA	P	T ACA	V GTG
Y TAT	S TCC	M ATG	P CCA	A GCT	N AAT	295 GGC	V GTG
W TGG	9 9	L	P CCG	P CCT	M ATG	G GGA	Q CAG
C TGC	C TGT	L	$\mathbf{Y}_{\mathbf{TAT}}$	N AAT	GGG	H CAC	E GAA

Fig. 1E

CAAGATGCTACATCAAAGGCAAAGAGGATGGACAGGCCCTTTTGTTTACCTTCCCATCCTCACCGATACTTGCTGATAG

734

DOFEELL CLIST

1919 2156 2393 2472 1366 1603 1682 1840 1998 2235 2314 1445 1761 2077 1208 1287 152 ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGTTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC CATGACTAAATCTTATCTTTTGATAGCAAATCCTTTTAAGAAACTGAACAATTGCTAAGGCTCAGCAATTTATACTC CAATGTCTGTGTAAGGTAAATTTTTGTTTGCCATTGAGCCCCACATTGGAATTCCTTCTGACGTCAACACTGACAATGCCT GAATCGACAGTAGCTGTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGGACTGGTAGACAGTTTCATAGGAAACTGCGG GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCTTGTGTCTCTGGGC TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCTTGTTTTACATAAGACAACAAAGCACAATGTCTGCTGTT CCTTTTTAAAATCAAGAAGCACAGTCAGAGCTGCCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC TCCCAGCCCATTCTCCTAATAGAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG GCTTTCCTCTGCAGGAATAGGAAAAGACCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCTCAG GCGTTTTATGAATCATCGTCTGGCTTTTTTTTAGTGCATGTATTGAAGTGAGGGTGTCCTTTGAGATCAGATGGGGAG TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCTTGGAGAGGAAGAGGGACAGCCAAAG AAACTCAGCAAAGCAAGACCAGCATTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCTCA GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAACCTACTTAGTTGCACAGATGACATAATCAAAAGTAGAAAAAAGAAG TGTAGTTAGAGATGCCATTTCCCCAGGTGAGAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAAACAGTA TGGAGTICTTTTCCCTTGCGTAGTTAGTCACGTTGATGTGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA TAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTTGGATCAGGCATCCAAAAGTGTCTTTGAGTGGACATT GAGTATTCTTTACCACCTACAAGACCAGGAGGCATGGTGTCATTCTCCATTGGGGTATTTATATGAGGTAGAGGTTCAG TACAATCAAGACGACTACATGGTCCAAACATTTCTTCTCTCTTTTTCACTTGTGGCTTTAACTTCCATTTCCTCCGTT GGTGGTCCAAGGGAAAACTTGGATATTCTCAAAGCAAGCCCAGCTCTTTTCAAGTCTTTTGTGGAGGACATTTGAATC CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACTTCGAAGAGAGACTTTCTATCCACCA TTGGACATCTATAGTTAAATAAGGCCATTAGAGGGGGAAATCTTTAAGTTAGGGGAAATTCTCTAAATGGAGACATT AGTGAACTCTGCGGGGGGTGGGGTGTCTCTACTCAGAGGGCTCCAACACCCTTTTCTTAGGTAGTTCTGGTGATGGGTT

Fig. 1F

DOVEMENT DINGER

2867 2788 2915 AGCTCTACTICTGTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCCACAGACATGAGGCCAGACTTGTGCATGCTCTTTC TIGGCAACACTIGGCTCATATITCTTGTTCTCTTTTGATAGAGTCCTGTTTCCTATGTATTAAAAAATAAAAGTG AATTTAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGCGC

Fig. 1G

Hum. Mur.	10 MRRQPAKVAALLLG : : : : : : : : : : : : : : : : :	20 :LECTEAKKHCW:.:::::::::::::::::::::::::::::::::::	30 VYFEGLYPTYY :::::::::: VYFEGLYPTYY 30	40 ICRSYEDCCG ::::::::: ICRSYEDCCG	50 SRCCVRALSI :::::::: SRCCVRALSI 50	20 30 40 50 60 70 LLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG ::.:::::::::::::::::::::::::::::::::
Hum. Mur.	80 VLFCCGAGFFIRRR :::::::::::: VLFCCGAGFFIRRR	90 (PPPLIEEPAFN ::::::::::::::::::::::::::::::::::::	100 VVSYTRQPPNP :::::::::: VVSYTRQPPNP 100	110 GPGAQQPGPP: .::::::::	120 YYTDPGGPGM :::::::: YYTDPGGPGM 120	90 100 110 120 130 140 MYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQV :::::::::::::::::::::::::::::::::::
Hum. Mur.	150 PPNSPQGSVACPPP :::::::::: QPNSPHGGTTYPPP	160 170 PAYCNTPPPPYEQVVKAK :.::::::::::::::::::::::::::::::::::	170 2VVKAK :::::: 2VVKDK 170			

Fig. 1H

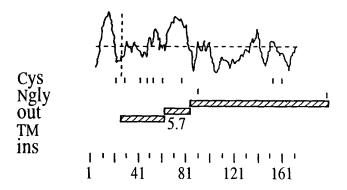


Fig. 1I

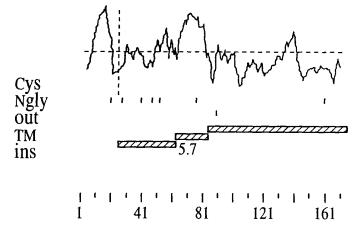


Fig. 1J

79	6 152	26 212	46	66 332	86 392	106 452	126 512
ATA	FTTT	H CAC	C TGC	Y TAT	CIT	Q CAA	G GGA
AAT	Q CAG	CIC	N AAC	L	S TCT	V GTT	PCCT
TGLI	L TTA	L TTA	I ATT	F TTT	H CAT	F TTT	D GAT
CTTCAGATTTAAAAAGAAACCTTTACTGAATCAGCTGAGTGTTAATAATA	G GGA	L TTA	Q CAA	V GTT	CIT	A GCC	$_{ m TTA}$
CAGO	C H G T	$_{ m LTA}$	R AGA	T ACA	GGA	K AAA	R CGC
GAAT	M ATG	CII	G GGG	S AGT	T ACA	P CCA	K AAA
TACI	GAT	Y TAT	T ACT	E GAA	L TTA	Y TAT	I ATC
CCTI	CAGG	C TGT	C TGC	P CCT	E GAA	V GTA	F TTC
SAAA?	AAGAA	T ACC	L CIC	F TTT	S AGT	Y TAT	N AAT
AAAG	CTGAACAGAAATCCAAGAACAGGGAT	V GTT	Q CAG	N AAT	E GAA	$_{ m CTG}$	N AAT
rta <i>i</i>	3AAAI	V GTT	C TGT	K AAG	N AAT	I ATT	N AAT
SAGAT	AACAG	L CTG	V GTT	P CCT	I ATA	N AAC	L CTA
CTT(rctg2	F TTT	S TCT	I ATT	$^{ m Y}$	S TCT	TTT
CGL	CTGAI	L	S TCG	S AGT	S TCT	N AAT	L CTA
AATGI	AATT(R CGA	C TGT	S TCG	I ATA	D GAT	F. TTT
GGA1	rgcc/	L CTA	GGA	L	N AAT	$rac{ ext{L}}{ ext{TTG}}$	Y TAT
CGTC	rtcti	C TGC	L	9 660	N AAT	$_{\mathtt{TAT}}^{\mathtt{Y}}$	L CTA
CACG	CCTT	P CCT	I ATA	$_{ m TTA}$	999	$_{ m L}$	H CAT
GTCGACCCACGCGTCCGGAAATGTCGTT	CGAATTTCCTTGCCAATTCTGAT	L CIG	E GAA	N AAC	T ACT	A GCA	R AGG
GTC	CGA	S TCT	K AAA	R CGT	L CTG	V GTA	$_{ m L}$

Fig. 2A

ogyassi na aga

146	166	186	206	226	246	266	286
572	632	692	752	812	872	932	992
F TTT	N AAT	D GAT	CII	V GTA	FTTT	N AAT	N AAT
S TCT	R AGG	L	N AAC	E GAA	P	R AGG	H CAT
V	Q	I	E	F	Q	I	S
GTA	CAA	ATA	GAA	TTT	CAG	ATT	AGT
Q CAG	$_{ m CTA}$	R CGG	CIT	A GCC	I ATA	R AGA	$_{ m L}$
N	N	Γ	H	N	A	S	I
AAT	AAT		CAT	AAT	GCA	TCA	ATC
Y	L	A	Q	S	E	N	$rac{ ext{L}}{ ext{TTG}}$
TAT	TTA	GCT	CAA	TCA	GAA	AAT	
Q	Y	V	F	P	I	K	H
CAG	TAC	GTT	TTT	CCA	ATT	AAA	CAT
$_{ m TTA}$	Q CAG	M ATG	GGC	V GTA	P CCT	L	K AAA
Y TAT	V GTT	GGT	S TCA	K AAA	N AAT	L	L
L	S	V	E	T	H	L	N
TTA	TCA	GTT	GAA	ACA	CAT		AAT
N	V	F	S	L	S	Y	N
AAT	GTT	TTT	TCA	TTA	TCT	TAC	AAT
R	L	T	I	N	L	E	I
CGT	CTA	ACC	ATA	AAT	TTG	GAA	ATT
CTT	D GAT	G GGT	R AGG	N AAT	S TCT	L	G GGA
N AAT	N AAT	S AGT	$_{ m L}$	S AGT	CII	N AAT	S AGT
L TTA	F TTT	GGG	I ATT			A GCC	F TTT
L	V GTA	L	N AAC	L TTA	R AGA	CIT	999
G	G	V	N	Y	L	G	D
GGA	GGA	GTC	AAT	TAT		GGA	GAT
K AAG	R AGA	TACT	N AAC	$_{ m ITG}$	S AGT	K AAA	R AGG
F	P	L	S	C	K	F	T
TTT	CCG		TCA	TGT	AAA	TTT	ACT
I	V	R	L	A	L	A	V
ATA	GTT	CGC	TTA	GCT		GCA	GTT

Fig. 2B

346 1172 386 1292 426 366 406 352 306 052 K AAG K AAA Q CAG T ACA K AAG N AAT S TCT E GAA $_{\rm TGT}^{\rm C}$ H CAC CIT C TGC V GTT A GCA CIT N AAC Y TAT H CAT L CTG $^{
m Y}$ GGA V GTC $_{\rm TGT}^{\rm C}$ M ATG I ATC N AAT I ATT I ATT R AGG $_{\rm TGT}^{\rm C}$ PCCT N AAC T ACA H CAT $_{
m LTA}$ N AAT P CCA E GAA S AGT I ATT N AAT E GAA $\overline{\mathbf{W}}$ L CTA PCCT 9 660 H CAT N AAC K AAG $_{
m L}$ T ACT S TCT N AAT $^{
m F}$ $^{
m TTT}$ PCCT T ACA I ATT I ATT K AAA L TTA T ACA A GCC N AAT T ACC S TCT CCC Y TAT VGTA $_{
m L}^{
m L}$ D GAT T ACA Ø R CGT V GTT V GTA S TCA L CTT N AAT N AAT AGT S K AAA A GCA L TTA A GCT $_{
m F}$ D GAT N AAT S TCT W TGG H CAT ACA Q CAG A GCA GCA N AAT Ø L CTA R AGA A GCT W TGG GAC L S AGC FTTT \Box S TCA A GCC GGC R AGA S TCT I ATT H CAT $\overline{\mathbf{W}}$ Ŋ M ATG S TCC I ATA $_{
m L}$ I ATT D GAC R CGT AAT Z M ATG R AGA $\frac{1}{1}$ R CGA M ATG V GTA L TTA N AAT L CTA N AAT S TCC AAT N AAC L CTT S TCA CIT Z A GCG I ATA GGC E GAG R AGA I ATC S TCT P CCA L TTG P TCA TACT ITA D GAT K AAG $\frac{L}{TTG}$ ഗ Ы S TCT T ACT $_{
m L}$ P N AAT L D GAT L TTA

Fig. 2C

TOPESTA STACTA

466 1532	486 1592	506 1652	526 1712	546 1772	566 1832	586 1892	606 1952
$_{ m TTT}$	I ATA	A GCT	E GAG	I ATC	R AGA	N AAC	I ATT
R AGA	Q CAA	D GAT	N AAT	$_{ m L}$	N AAT	$^{\mathrm{C}}$	Q CAA
GGT	V GTG	N AAT	$_{ m ITG}$	F TTT	E GAA	I ATT	K AAA
A GCT	PCCT	P CCG	K AAG	I ATT	R AGG	S TCA	H CAT
PCCT	L TTA	L CTA	EGAG	I ATC	S TCA	A GCC	L
S TCA	V GTG	A GCT	V GTT	$_{ m L}$	N AAC	TACT	R CGA
T ACT	A GCA	S AGT	E GAA	V GTT	E GAA	V GTA	I ATT
P CCT	T ACA	N AAC	CAA	$_{ m TGT}$	S TCA	N AAT	Q CAG
I ATT	TACT	K AAA	T ACA	A GCT	A GCA	Y TAT	E GAG
R CGA	E GAG	E GAA	$^{ m C}_{ m TGT}$	L TTA	K AAG	R AGG	$rac{ ext{L}}{ ext{TTG}}$
E GAA	L TTA	$_{ m ITG}$	I ATT	I ATC	L CTA	A GCA	GGC
W	P CCA	N AAC	$_{ m CTA}$	F	K AAA	S TCA	P CCT
F	N AAT	$_{ m TTG}$	S TCT	F TTT	O CAA	Q CAG	S AGT
TACT	GGT	TACC	T ACA	A GCT	K AAA	Y TAT	E GAA
I ATT	FTTT	V GTT	K AAA	L CIA	F TTT	F TTT	L CTA
N AAC	A GCC	S TCT	999	$_{ m ITG}$	Q CAG	S AGC	S TCT
E GAG	N AAT	T ACT	S TCA	I ATT	V GTT	$^{ m Y}$	N AAT
TACT	E GAG	TACT	M ATG	D GAC	V GTT	$_{ m TAC}^{ m Y}$	P CCA
E GAG	Q CAA	$_{ m CTT}$	S TCA	F TTT	K AAA	E GAA	S TCC
T ACT	$_{ m T}$	Q CAA	A GCT	A GCT	$^{ m Y}$	L	TACT

Fig. 2D

NOTERLI NIIGOI

623 2003	2082	2161	2169
V I L F E H S A L * GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA	CTCAACTAAATATTGTCTATAAGAAACTTCAGTGCCATGGACATGATTTAAACTGAAACCTCCTTATATATA	TTTAGTTGGAAATATAATGAATTATGAGGTTAGCATTATTAAAATATGTTTTTAATAAAAAAAA	2169
V P E N E A Q GTT CCT GAA AAT GAG GCA CAG	'AAGA	ATTA	
E GAG	CTAT	AATGA	
N AAT	\TTG1	\TAT?	
E GAA	AAAT!	3GAA.	7.)
P	ACTE	GTTG	ລອວລອອລຣ
V GTT	CTCA	TTT	ງງວງ

Fig. 2E

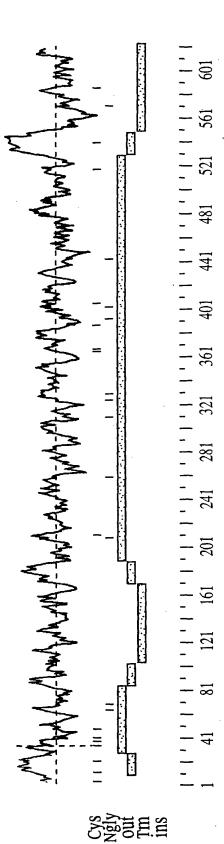


FIG. 2F

DOZEETT DITOCI

10 50 60 SVGWQMLSLSLGLVLAILNKVAPQACPAQCS-CSGSTVDCHGLALRSVPRNIPRNTERLDLNG :. :::::::::::::::::::::::::::::::::::	70 80 100 110 120 130 Slit NNITRITKTDFAGLRHLRVLQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPELLFLGTAKLYRLDL :::::::::::::::::::::::::::::::::::	140 150 160 170 180 200 Slit SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNHMPKLRTF .:: .::::::::::::::::::::::::::::::::	210 220 230 240 250 260 270 RLHSNNLYCDCHLAWLSDWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCP ::VAVA
10	70	140	210
Slit MRGVGWQMLSLSLGLV	Slit NNITRITKTD:	Slit SENQIQAIPR	Slit RLHSNNLYCD
: : : : : : : 325 MCGLQFSLPCLRLFLV	::: :	325PGI	325

Fig. 20

DOVESCHI COLIOCI

) APDAF) !IAKG) AKEQY	TGIF
340 SNNQISELA: ::::: SNNNI	410 YDNKLQT	480 KKFRCSAI	550 NNEFTVLEAT .:.: :: . SNAFEVLKS-
330 KLRRIDLSNNQI :: .:::::: -LRILDLSNNNI	0 400 DAFQDLHNLNLLSI:::::::	470 NKRIGQIKS	540 TAELRLNNN ::
280 330 340 Slit AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF ::::::: 325LRILDLSNNNI	350 360 370 380 390 400 410 QGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKG :: ::::::::::::::::::::::::::::::::::	420 430 440 450 460 470 480 TFSPLRAIQTMHLAQNPFICDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY :::: 210	490 540 550 550 530 540 550 FIPGTEDYRSKLSGDCFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIF .:.:: 220
310 EIRLEQNTIK 	380 LQLLLLNANK 	450 ADYLHTNPIETS :: :: YLGSN	520 STTVDCSNQK N
300 PTNLPETITE	370 KSLFEGLFS1	440 SDCHLKWLADY:	510 ACPEKCRCEG
290 DCRGKGLTE1	360 LYGNKITELE :: ISE	430 MHLAQNPFIC	500 KLSGDCFADI
280 AACTCSNNIV	350 QGLRSLNSLV :: LR	420 TFSPLRAIQT	490 FIPGTEDYRS
slit 325	Slit 325	Slit 325	Slit 325

Fig. 2H

norectt niidon

560 570 580 600 600 610 620 Slit KKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLRSNRITCVGND :::::::::::::::::::::::::::::::::::	630 640 650 660 670 680 690 SFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSTLNLLANPFNCNCYLAWLGEWLRKKRIVTGNPRCQKP .: : : .:. GFSGINNLKHLILSHND	700 710 720 730 740 750 760 YFLKEIPIQDVAIQDFTCDDGNDDNSCSPLSRCPTECTCLDTVVRCSNKGLKVLPKGIPRDVTELYLDGN :	770 780 800 810 820 830 QFTLVPKELSNYKHLTLIDLSNNRISTLSNQSFSNM-TQLLTLILSYNRLRCIPPRTFDGLKSLRLLSLH ::::::::::::::::::::::::::::::::::
560 lit KKLPQLRK:::325LRR	630 Slit SFIGLSSV .: :	700 Slit YFLKEIPI 325	770 Slit QFTLVPKE :.:. 325 TFSLL
S1 3	S1 3	S 1	S .

Fig. 21

DOVERSA CALCOA

			r	
900 OKLLLTTPSK	970 NPCKHGGTCH :: -PSMRG 390	1040 EEKLDFCAQD	1110 EGYSGLFCEF	
890 RCAGPGEMAI	960 CDVPIHACISI : : CQNP	1030 CPPEYTGELC	1100 AVNGYTCICP	TSSIN
880 KSEYKEPGI <i>P</i> : AS	950 CPYGFKGQDC	1020 'DGINNYTCLG	1090 KCKNGAHCTD <i>i</i>	;SI
50 860 870 SALSHLAIGANPLYCDCNMQWLSDWVKSE ::::::::::::::::::::::::::::::::::::	20 930 940 950 960 970 CNPCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH : : : : : : : : : : : : : : : : : : :	90 1000 1010 1020 1030 1040 GFEGENCEVNVDDCEDNDCENNSTCVDGINNYTCLCPPEYTGELCEEKLDFCAQD : : :	60 1070 1080 1090 1100 1110 GEKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSGLFCEF	
860 JAIGANPLYCI :	930 SNPCKNDGTCN	1000 NCEVNVDDCEI	1070 CTPGYVGEHCI	
850 FNDLSALSHI ::::: SSLIHI 350	920 ILAKCNPCLS :	990 :: :	1060 LTPKGFKCD	
840 850 870 880 900 Slit GNDISVVPEGAFNDLSALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPGIARCAGPGEMADKLLTTPSK ::::::::::::::::::::::::::::::::::::	910 9 Slit KFTCQGPVDVNILAK 325SAITLNI	980 LKEGEEDGFWCICAD : RALRYI	1050 LNPCQHDSKCILTPK	
Slit (Slit 325	Slit 325	Slit	325

Fig. 2.

1130	1340 1350 1360 1370 EPCHKKVCAHGTCQPSSQAGFTCECQEGWMGPLCDQRTNDPCI :
1120 Slit SPPMVLPI 325VSI Slit ITLQIATI 1260 Slit LSVDGGNI 325 TSV 490	1330 Slit PMQTGILPGC ::: . 325 NEAFDILLA- 530

Fig. 2K

1460	Slit SCKCLEGHGGVLCDEEEDLFNPCQAIKCKHGKCRLSGLGQPYCECSSGYTGDSCDREISCRGERIRDYYQ	: .: .:: RENRL-EYY- 570		GCTRCVS	•	·LFEHSAL	620
1450	GDSCDREISC	 NS	1520	'VDEVEKVVKC	••	QIVPENEAQVI-LFEHSAL	610
1440	PYCECSSGYT	SEI	1510	SFECTDGSSF	•	 	
1430	KCRLSGLGQ	.: . KLKA	1500	SPLRSKRRKY	•••	SLEQIRLHK-	009
1420	PCQAIKCKHO	.: :: .: .: .: .: .:::	1490	GGCAGGQCC	•••••••••••••••••••••••••••••••••••••••	ITSPNSLESP(590
1410	LCDEEEDLFN	 -	1480	K-KVSRLECR	•	RYNVTASICN	580
1400	SCKCLEGHGGV	1 1	1470	Slit KQQGYAACQTTK-KVSRLECRGGCAGGQCCGPLRSKRRKYSFECTDGSSFVDEVEKVVKCGCTRCVS	:	325SFYQSARYNVTASICNTSPNSLESPGLEQIRLHK	
	Slit 9	325 AC-		Slit 1		325 -	

Fig. 21

CONTROLL ORLCOL

70 TT	1	140 GGT	210 CGC	280 CGC C
'ATTA	! ! !	1 3CGCG	2 3ATGC	28 ;CACCG :::
10 20 30 40 50 50 70 Slit cagagcagggaggggggggggggggggggggggggggg		80 90 100 110 120 140 TTGTGCACATTTTCCCTGGCACTCTGGGTTGCTAGCCCCGCCGGGCCACTGGGCCTCAGACACTGCGCGGT	150 160 170 180 190 200 210 Slit TCCCTCGGAGCAGCTAAAGAAAGCCCCCCAGTGCCGGCGAAGGAGGGGGGGG	220 230 240 250 260 270 280 GGCGTTGGCTGGCAGATGCTGTCCTGTCGCTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGC ::: GTCGACC
CTTG		13 TCAG2	2(27 3AACAA
50 TACTG		0:00	10 'AGGCC	TCCTG
GCTCI		120 GCACTG	190 GAAGGA	260 GGCGAT
40 GAGTGG			0 GCGAG	0 GTGCT
4 GCCTG	! ! ! !	110	180 TGCCGG	250 GGTTAG
30 GCGTGT	 	0 TGCTA	0 CCCAG	0 GCTGG :
3 GGAGG	 	100 TGGGTT	170 AAGCCC	240 CTGTCGC ::::
) CGGTG	 	CACTC) AAAGA:	GTCC
20 sagggc		90 3CTGGC	160 AAGCTA	230 SATGCT
) STGGA(! ! !) TTTC() SCAGC?) 166CAC
10 scagg	 	80 CACAT	150 CGGAG	220 TGGCT
CAGAG	 	TTGTG	TCCCT	
Slit	325	Slit 325	Slit 325	Slit 325

Fig. 2M-1

DOYMELL CLIODI

0 1 1	O the L	O 4. I	0 () •• ()
310 340 350 330 340 350 350 340 350 GTGCTCTTGCTCGGGCAGCGTTGACGGGCTGGCGCTGCGCAGCGTTGTCACGGGCTGGCGCTGCGCAGCGTTGTCACGGGCTGGCGCTGCGCAGCGTTGTCACGGGCTGCGCAGCGTTGTCACGGCTTGCACGCAC	370 380 390 400 410 420 CGCAACACCGAGAGACTGGATTTAAATGGAAATTAACATCACAAGAATTACGAAG	440 450 460 470 480 490 TTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAA ::::::::::::::::::::::::::::::::	500 510 520 530 540 550 560 Slit GAGGAGCATTCCAGGATCTTAAAGAACTAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCC ::::::::::::::::::::::::::::::
GCA	LTAC	CCATTG:::.CCTTTA	CTGT :
0 CTGC	0 GAAT 	0 CACC CC 50	0 CAG(
340 3GCGC	410 ACAAG	480 LTAGC	550 3CTTC
GCIC	ATC/	AGAT : A	TCAC .:. ACG-
330 ICACGG :::: -CACG-	400 ATAAC 	460 470 TCTTCAGCTTATGGAGAATAA ::::::::::::::::::::::::::	540 TTAAACAGAAATCAC ::::: TTAATAATACG- 80
33 GTC <i>I</i> ::	4(AAA1	47 GAGA	5, ACA(.T
3ACT	4TGG	rarg : rtaa 40	TTAA :::: TTAA
320 AGTG(390 TTAA	460 AGCT: :::	530 GCGT'
SACA	3ATI	TTCP	ACTG
CAG	CTG	GTTCT ::::: GTTCT 30	0 GAGAG ::::: GAGTG 70
310 CGGG	380 GAGF	450 AGAC	520 AACTAGAGAGA :.:: :::: AGCT-GAGTG-
GCT.	CCGA	rcta	SAAC ::: -AGC
TCTT	ACA(ACA1	AAA(
300 3TGC	370 3GCA	440 LTAG	510 TCTT :: TC
GCAC		GTCI	51 CAGGATCT ::::: CTGAATC-
	360 GCCCAGGAATATCCCC ::.::::: CCGGAATGTC	430 ACAGATTTTGCTGGTC	0 ICCA CI
7300 GCCC	360 CCAGGAATAT :::::::: CCGGAAATGT 20	430 TTTG:	500 SCATT
3CGT	CCAG	AGAT	GGAG
AG(AC	GA
290 Slit AGGCGTGCCCGGCGCA	Slit 325	Slit 325	Slit 325

Fig. 2M-2

IOPEKKII IIIIGII

630 3GCAATC :: 3G	700 AGCTGTA ::. GTT	770 TTACTAG	840 CCTGTAT :: AT 200
620 AAAACCAAATTCAG :::.::::::: AAATCCAAGAACAG 120	690 ACCAGATC:	760 TAACAACA'	830 TCAAACAA
580 620 630 630 630 630 630 630 630 630 TGGGACTGCGAAGCTATACAGGCTTGATCTCAGTGAAATCCAAATTCAGGCAATC ::::::::::::::::::::::::::::::::::	650 660 700 700 CGTGGGGCAGTTGACAAAATTTGCAACTGGATTACAACCAGATCAGCTGTA .::::::::::::::::::::::::::::::::::::	720 730 740 750 760 770 TCAGGGCTCTCCGGGACCTGGAAGTGCTCACTCTCAACATAACAACATTACTAG ::::::::::::::::::::::::::::::::::::	790 800 810 820 830 840 TTTCAACCATATGCCTAAACTTAGGACTTTTCGACTGCATTCAAACAACCTGTAT :: .:::: TTGTTACCTGTTATCTTTT
600 CAGGCTTGATC :.:. CTGA110	670 AAAAATTTGC? .:.:::	740 3GAAGTGCT(::: TGC	810 CTTAGGACTTTT .::::
590 CTGCGAAGCTATACAGG : ::: ::::: CCAATTCTGATCTGA 110	660 TTGACATAAA	730 CCGGGACCTG .:: GCCT- 160	800 ATGCCTAAA(::
580 TGGGACTGCGAA ::::::: TGC-CAA	650 3GTGGGGCAG	720 rcagggcrcr ::::	790 80 TTTCAACCATATGC :: .:::. TTGTTACCTGTTA-
570 TGAGTTGCTGTTTCT1 : :::: TTTTCT1	640 CCAAGGAAAGCTTTCC	710 TTGAAGATGGGGCAT: :: TT	780 ACTTTCTGTGGCAAG:::::-::
Slit 3	Slit (Slit 335	Slit 325

Fig. 2M-

nareett niidh

910 AGT :T	980 TGG :::	1050 CAAT	1120 ATAC .:.: 'TTTC
9. .: ::	GCAG :: GCAC	1 ,AAC	SAAA
TACA::::	980 TCTGCAGTGG ::::::: TCTGCACTGG 250	TAGC ••••	ACAG; ::: ACAG' 320
900 CTGT ::: -TGT' 230	970 TTG	1040 CCCTG: :: ACTTZ	11110 CATC
900 TTGGTCTGTACAC' ::::. ::::: TTGGA-TGTTCG-'	AAT'	1040 GTACCTGTAGC ::: :: .:: GTAACTTAGGC 280	1 :ACC :- -A
.: .: -TT(GAG	CTG:	0 CAGAGA : . : . : CTGAAP
890 TCGG	960 AAAC	1030 GCCGC	1100 TTCC/ ::::.
6CCJ	CAAZ	1(CTG(1100 1110 1120 ATCTTCCAGAGACCATCACAGAAATA ::::::::::::::::::::::::::::::::
) CAAAGGCC ::: .: -AAATAC- 220	GTT	20 ACTGCC ::::: ACTGCC 270	`AAA` :
880 GCCA :	950 CGAG	1020 GCACTGCC ::::: ACTGCC 270	1090 CCCAC
TTCC	AGCC	1. TTG(I CC I
1 - L	TGT	GTT	80 CTGAGA ::.:: CTAAGA
870 GACT	930 940 950 960 970 980 ACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAACGAGAATTTGTCTGCAGTGG ::: ::::::::::::::::::::::::::::::	1000 1010 1020 1030 1040 1050 GGCTCCTTCTTGTAGTGTTTTGCACTGCCCTGCCGCCTGTACCTGTAGCAACAAT ::::::::::::::::::::::::::::::::	1070 1080 1090 1110 1120 GGGAAAGGTCTCACTGAGATCCCCCACAAATCTTCCAGAGACCATCACAGAAATAC : :::::::::::::::::::::::::::::::::::
		1 (TTG:	
D I		TLT.	O AAGGTCT :: -TATTC-
860 CTGG	930 CTGA	1000 GCTCC	1070 GGAA?
3 3 3 3 5 5 7 8	CACC	1 (TGG(1(TGG(.:
CCT	011000 11000 11000	990 CCAGTCATTTAT :::::.:	060 ACTGTCGT :: ::: -CTTTCGA
850 GCCACC :::: CCAC?	 2000 300	990 TCAT	1060 GACTG' ::
ACTC	TGGG(9 CAGT ::. -AGA 260	1 TAG
850 860 910 910 TGTGACTGCCACCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACACTCAGT ::::::::::::::::::::::::::::::::::::	920 GTATGGGCCCCTCCC ::.:: GTTTGTC 240	990 TCACCAGTCATTTAT :::::.: GAGACAAATTA	1060 ATCGTAGACTGTCGT ::::: CTTTCGA
Slit I : 325 I		Slit T 325 G	Slit <i>1</i> 325 -
S1: 3;	Slit 325	33	S1 3

Fig. 2M-

DOVERT DITODA

1160 1170 1180 1190 CTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT :::::::::::::::::::::::::::::::::::	1210 1220 1230 1240 1250 1260 TCAGATCTCTGAACTTCCAAGGACTACGCTCTCTGAATTCA :::::::::::::::::::::::::::::::::	1320 1330 TGTTTTCCTTACAGC :.::::::: TAATTCTAACA 410 420	1350 1360 1370 1380 1400 1400 CCAACAAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCACAACTTGAA ::::::::::::::::::::::::::::::::::
1180 TAAAAAGC ::::: TATAAATG 360	1250 CTACGCTC::::	1320 GACTGTTTT :: TAAT	1390 AGGATCTCC ::: AGG
1170 118 "TCTCACCATATAAAAA(: .:::::::::::::::::::::::::::::::	1240 TTTCCAAGGACTAC::::::::::::::::::::::::::	0 AGTTTATTTGAAG : ::::::: ATTGTATTTGGA-	1380 SATGCTTTTCAGGA : : : : : : :
1160 CCTGGAGCTTTCTC ::::. : -CTGGGAATAATA7	1230 CACCAGATGC	1300 CCCCAAAAGT' : : ATT	0 1370 TGCCTTCGGGTAC ::::: :
1150 AGTCATCCCT	1220 TCTGAACTTG	1290 TCACAGAACT : : AGC-	1360 GATAAACTGC ::
1140 CACAATCAA	1210 AATCAGATC	1280 3aaataaaa 	1350 IGCCAACAA(: :::::: I-CCAAAA-
1130 1140 1150 1160 1170 1180 1190 Slit GTTTGGAACACAATCAAAGTCATCCTCCTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT :::::::::::::::::::::::::::::::::::	1200 t TGACCTGAGCAATAA' :.:: 5 TAAC	1270 1280 1300 1310 1320 1330 t CTTGTCCTCTATGGAAATAAAATCACAGAACTCCCCCAAAAGTTTATTTGAAGGACTGTTTTCCTTACAGC ::::: 5 CTTGTTAATTCTAAACACATTGTATTTGGATAATTCTAACA 400 420	1340 t TCCTATTATTGAATG : ::.:.:: TTCTGTATGTATAT-
Slit 325	Slit 325	Slit 325 39	Slit

Fig. 2M-5

DATESTA DIAGOA

1410 1420 1430 1440 1450 1460 1470 CCTTCTCTCCCTATATGACAAGGCTTCAGACCATCGCCAAGGGGACCTTTTCACCTCTTCGGGCCATT ::::::::::::::::::::::::::::::::::	1480 1490 1510 1520 1530 1540 Slit CAAACTATGCATTTTGGCCCAGAACCCCTTTATTTGTGACTGCCATCTCCAAGTGGCTAGCGGATTATCTCC ::::::::::::::::::::::::::::::	1550 1560 1570 1580 1590 1600 1610 ATACCAACCGATTGAGACCAGTGCCCGTTGCACCAGCCCCGCCGCCTGGCAAAAAAATTGG ::: GTAATTTATATTT 550	1620 1630 1640 1650 1660 1670 1680 Slit ACAGATCAAAAGCAAGAATTCCGTTGTTCAGCTAAAGAACAGTATTTCATTCCAGGTACAGAAGATTAT :::::::::::::::::::::::::::::
Slit CCTTCT :::: 325 T-TTCT 470	Slit CAAAC7	Slit ATACC?	Slit ACAGA'
	:::::	.::	::::.
	325 CAAAC	325 GTA	325 ACAGT

Fig. 2M-6

DOVECETT OTTOOK

1750 3GAACCA	1820 AGTTGCG	1890 acgtaaa	1960 GTAAATG
1740 CGCTGTGAA	1810 ACACTGCAG; :::: -CACTG	1880 TTCCTCAATT::::: TACCT	1950 GCATCTGGT ::::: -CTTCGG
1730 rgaaaagtgt	1800 ATTCCCCAGT: ::::-	1870 FTAAGAAACT' : T	1940 ATTTGAAGGA
1720 GGCTTGCCCT : .G	1790 .ccggagcac <i>i</i> :::. GGAA	1860 CAGGAATCT7 .:: TGG	20 1930 ATATTGAGGAGGAGCA :::::::::. TTGTTGGTATGGTTGCT
1710 TTGCGGATCTGG :::::::	1780 CAACAAAATC ::: CAAA	1850 TTGGAAGCCA :::::: TTGGGAG	1920 CAGATATTGA .::::.
1700 3GAGACTGCT	1770 AATCAAAAGCT :::::: AATCTA	1840 ATTTACCGTG .:: TCC	1910 1920 1930 1940 1950 1960 CAATAAGATCACAGATATTGAGGAGGAGCATTTGAAGGAGCATCTGGTGTAAATG
1690 1700 1710 1720 1730 1740 1750 Slit CGATCAAAATTAAGTGGAGACTGCTTTGCGGATCTGGCTTGCCCTGAAAAGTGTCGCTGTGAAGGAACCA :::::::::::::::::::::::::::::	1760 1770 1780 1790 1810 1820 CAGTAGATTGCTCTAATCAAAAATCCCGGAGCACATTCCCCAGTACACTGCAGAGTTGCG :::::::::::::::::::::::::::::::::	1830 1840 1860 1890 1890 1890 1890 1890 1890 1890 189	1900 ATAAACTTTAGCAAC
Slit CC 325 -(slit C2 325	Slit To 325 -	Slit A 325 -

Fig. 2M-7

1976511 Dilini

2030 TCAA :	2100 TGTG	2170 TCTT	2240 :GGCT :
1970 1980 2000 2010 2020 2030 Slit AAATACTTCTTACGAGTAATCGTTTGGAAAATGTGCAGCATAAGATGTTCAAGGGATTGGAAAGCCTCAA :::::: :::::::::::::::::::::::::::::	2050 2060 2070 2080 2090 2100 SAAGCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGTTCTGTG ::::::::::::::::::::::::::::::	2110 2120 2140 2150 2170 CGTTTGCTTTCTTTGTATGATAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCATTCTT ::::::GCTTTC	2180 2230 2240 2240 2220 2230 2240 TATCTACTCTAAACCTCTTGGCCAATCCTTTTAACTGTAACTGCTTGGCTTGGTTGG
2010 GATGTTCAAG	2080 TGACAGTTTCA:::: TATCAGAATCA:	2150 CAGGGGCATT	2220 CTACCTGGCTTG:::::
2000 GTGCAGCATAA	2060 2070 2080 AATAACCTGTGGGGGAATGACAGTTTCAT:::::::::::	2140 TACAGTTGCAC	2210 AACTGTAACTG
1990 TTTGGAAAAT	2060 CGAATAACCT(::::: AATAAC;	2130 ATCAAATTAC'	2200 CAATCCTTTT ::.:: -AAACCTT
1980 ACGAGTAATCG :::::: GATTTATC- 690		2120 TTGTATGATA	0 2200 TAAACCTCTTGGCCAATCCTTT :::::::::
1970 AAATACTTCTTA ::::: ATACTT	2040 Slit AACTTTGATGTTGA(::: 325 AAC	2110 CGTTTGCTTTCT ::::: GCTTTC-	2180 TATCTACTCTAA :
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-8

COPESIA OHIGH

Fig. 2M-9

DOVERSIA STAGOL

2530 2540 2550 2560 2570 2580 2590 CTCTCCAACTACAACATTTTAACATTATAGACTTAAGTAACAACAGAATAAGCACGCTTTCTAATCAGA ::::.:.::::::::::::::::::::::::::	2610 2620 2640 2650 2660 2660 2600 2600 26000 200000	2670 2680 2700 2710 2730 2730 CACCTITGAIGGAITAAAGICICITICGAITACITICICITACAIGGAAAIGACAITICIGITIGIGCCIGAA :::::::::::::::::::::::::::::::::	2740 2750 2760 2770 2780 2790 2800 GGTGCTTTCAATGCATTATCACTTTACTGTGATTGTA :::::::::::::::::::::::::::::
2550 2560 2570 TATAGACTTAAGTAACAACAGAATAAG ::: ::::::::::::::::::::::::::::::::	2640 ACAACCGTCT :::.	2710 ATGGAAATGAC .:: .::: TTGTTAAAGA- 1030	2780 :GGAGCCAACC
2560 CTTAAGTAAC :::::::	2620 2630 CACCTTAATTCTTAGTT ::::::::	2700 ACTTTCTCTAC?::::::::::::::::::::::::::::	2770 TCTAGCAATT ::::::
2550 CACTTATAGA(:: TTAGGA·	2620 CCTCACCTTA ::::	2690 CTTCGATTAC :: . :: TCTGACAC	2750 2760 CTTTCTGCATTATCACACACACACACACACACACACACAC
2540 AAACATTTAA ::.: ATTCAAGAA- 920	2610 TGACCCAGCT :.: TAA	2670 2680 CTTTGATGGATTAAAGTCT :::::::::-:	2750 GATCTTTCTG ::. ::: \GAAACAG
2530 CTCTCCAACTACAAA :::::	2600 GCTTCAGCAACA . :: : ::.: AATTAATAATCT 960		2740 GGTGCTTTCAATGAT : :: ::: GTTAGATAGAA
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-10

DOYGESII DIIJOII

2870 GCTGGTCC :::: AGATCC	2940 CTGTGGAT	3010 FAATAGTG :	3080 CCAATTCA :::: ATTCA
2860 GCTCGTTGTGC : ::: CTTTGAA-	2930 CTGTCAAGGTCC ::::: CTGTCAT	3000 TGGCACATG:	3070 TGTGATGTC
2850 GCCTGGAATT ::: GCAT	2920 29 AAATTTACCTGTCAA :::::::: TAATCTGTCAT 1130	2990 GTAAAAATGA : G	3060 GGGGCAGGAC : TG
0 2840 28 TCGGAATATAAGGAGCCTG : :::::::::::::::::::::::::::::::::::	2910 rcctccaaa	970 2980 TGCCTATCAAATCCGTG' :::: : ::::-: -GCCTTGCATCCAAG	3050 ATGGTTTCAAGGG ::::. : TTCATTG-
2830 GTGAAGTCGGA : ::	2900 :ACTCACAAC:	2970 CCCTGCCTA' :::. GCCTT(3030 3040 3050 3060 3070 3080 TACCGATGCACCTGTCCATATGGTTTCAAGGGGCAGGACTGTGATGTCCCAATTCA .::: AGCCGTTGTCTTCATTG1180
2820 .TCCGACTGGG	2890 ATAAACTTT1	2960 TAAGTGTAAC	3030 ACTTTTACCGATGC/ ::::.
2810 2850 2870 2870 2870 2850 2860 2870 Slit ACATGCAGTGACTGGGTGAAGTCGGAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCC :::: :::::::::::::::::::::::::::::::	2910 2920 2930 2940 Slit TGGAGAAATGGCAGATAAACTTTTACTCACAACTCCCTCC	2950 2960 3000 3010 GTCAATATTCTAGCTAAGTGTAACCCCTGCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTG : ::::::::::::::::::::::::::::::::::	3020 ATCCAGTTGACTTT .::: :: GTCCTTA
Slit ACZ :: 325 ACZ 1090	Slit TO : 325 T	Slit G	Slit A 325 G

Fig. 2M-1

3150 TGGATTC :: :: TGCAAAC 1230	3220 AGATAATG :	3290 3AGTATAC	3360 ATTCAAAG
3140 3150 AGGAGAAGAAGATGGATTC ::.::::::::-::-:-:	3210 ATGATTGTGAA	3280 TTGCCCACCTC	3350 rgccagcac <i>g</i> ?
3130 .:: :::: .CTTG	3200 GTCAACGTTGA GENERAL :	3270 ACACATGCCTTTGC ::::::::::::::::::::::::::::::	30 3340 AGGACCTGAACCCCT ::: ::::GTCAGAATCCCC- 1290
3120 AACTTGCCACTT. ::.:::	3190 AATTGTGAAG	3260 TTAATAACTACAC: ::::: TCTTCA-	3330 TGCCCAGGAC(: ::: TTGTC/
3110 aacarggagg	3180 IGAAGGAGAA	3250 GTCGATGGCATT ::::: TAGCAT- 1260	3320 GCTGGACTTCTGTG :::.: TCTAAACATCTATT 1280
3100 ACCCATGTA? ::.:.	3170 TGATGGATT	3240 TCTACATGT(.:	3310 3AGGAGAAGC' : :TC'
3150 3140 3150 3150 3150 3140 3150 3140 3150 3140 3150 3140 3150 31it TGCCTGCATCAGTAACCATGTAAACGAACATGGAACTTGCCACTTAAAGGAAGG	3160 3170 3180 3190 3200 3210 3220 TGGTGTATTTGTGCTGATGGATTTGAAGGAGAAAATTGTGAAGTCAACGTTGATGATGTGAAGATAATG : :::::: TTTTGGGC	3230 3240 3250 3260 3270 3280 3290 Slit ACTGTGAAATAATTCTACATGTGTCGATGGCATTAATAACTACACATGCCTTTGCCCACCTGAGTATAC :::: ::::::::::::::::::::::::::::::::	330 3340 3350 3360 t AGGTGAGTTGTGAGGAGACTTCTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAG ::.::::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

1290 **Fig. 2M-12**

DOVERLI DIIIOLI

о U I	0 U &	o v v	0 U U
3430 ATCG	3500 CTATAC ::: ATAA 1360	3570 TACC:	3640 ATGTC ::::
GAC	3GCT	CTCG	1ATA ::::
CTGC	0 AACC	O TCCCT :: :: TCACA	30 3640 AGCCAATATGTC :::::: CAA-ATGGC 1450
3420 ACAC'	3490 GTGA	3560 TCCT(:::	3630 .TGAG
3TGA	[GCA	3560 ATGGTCCTCCCTC ::.:::: ATATTCATCACAP 00 1410	raaa
0 TAGC :. TT	0 AGA1 	0 CCCAT(:::CAT;	O GAA:
3410 TACGT ::::: TACGT	3480 CACA(:::	3550 CCAC	3620 GTCAG
3410 AGGGTACGTA ::::: TTACGTT 1320	34 3CCCACTGCA : .: :: CATCTTCA	540 3550 3560 357 GAGTTTTCTCCACCCATGGTCCTCCCTCGTAC ::::::::::::::::::::::::::::::::::	3610 3620 SAGCTCAGTGTATCGTCAG ::::::::::::::::::::::::::::::::::::
0 CCA(0 CCC/ - CA/	40 AGTT' TAAAJ	610 AGTGTA' ::: AAAGTA' 0
3400 CACAC	3470 3GAGC	3540 3TGAGT : 133	3610 CTCAGT(:::.:. CATAAA()
CTG(:.: CAG2	AAC(ICT(AGCTC::-GCA1
3370 3380 3400 3410 3420 3430 TGCATCCTAACTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAACACTGCGACATCG ::::::CATCCATGCGTGGCAGAGCATTACGTT	3440 3450 3460 3470 3480 3490 3500 ATTTTGACGACTGCCAAGACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATAC :::::::::::::::::::::::::::::::::	3530 CAGTGGCTTGTTC : ::: ::: CTTGGGCT-GTT- 1380	Ö i
3390 AATGT(:: GT(1310	3450 3460 AAGACAACAAGTGTAA : . : : : . : : : : : : : : : : : : : :	3530 GTGGCTT ::: TGGGCT-(3600 CAGAAT
TCA	CAA	AGT.	: : : : : : : : : : : : : : : : : : :
30 3GAT	3450 AAGACAA :.:::: ATTACAA	20 ITAC :	90 36 GATTGTCAGA ::: ::: GATGGCCTG- 1430
3380 AAGGG	3450 AAGAC, :.:: ATTAC, 134	3520 AGGTT: :: AG	3590 TTTGA:::GA:
CCA		0 CCCCGAAGG ::.:: CCAGAG- 1370	raat :::: raat
70 AACJ : TGC-	40 GAC1	3510 ATGCCCC :: CCZ	3580 AGCCCTGTGATAAT': : : ::: TACTGCGCTAAT
3370 CATCCTAAC :::::::: CATCCATGC	3440 GACGA(.::	35 TAT : :	3580 CTGTG; ::::
GCAT ::: -CAT	344 ATTTTGACG :::::: ATATTAAC- 1330	GTGCAT.:::	GCCC .: AC
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-1.

3710 AAAGAGTC ::. TGGGAA 1500	3780 CAGATGAA .:.: TTGGTAA- 50	3850 GGGCGTGTTC :::: GCAAATAC 1590	3920 SATGGAAA : :
3690 3700 37 GTGTGAATTTTATAAACAAAGAG ::::::::::::::-:::::	3740 3750 3760 3770 3780 TTCGGCCTCAGACGACATAACACTTCAGATTGCCACAGATGAA :::.::::::::::::::::::::::::::::::::	3840 CTATCGGGG(::::	900 3910 GTGGAGACAATCAATGAT :::::::::::::::::::::::::::::::::
3690 AGTGTGAAT ::::: TGAGAAC	3760 .TAACACTTCA.::::::::::::::::::::::::::::	3830 GCGGTAGAACTCTAT :::::::::::::::::::::::::::::::::::	3900 AGTGTGGAG . :::: TTGGAA
3680 AAATTGGTT ;	3750 AGACGAACA'::::::::::::::::::::::::::::::	3820 GACCATATCGC :: :: CAGC 1570	3880 3890 3 CCAGCTTCTGCCATTTACAGT : :: :::::
3660 3670 3680 3690 3700 3710 ATCAGGGAGAAAAGTGTTAGTTTGTGTTTTATAAACAAGAGTC ::::::::::::::::::::::::::::::::::::	3730 3740 3750 3760 3770 3780 TTCAGCCAAGGTTCGGCCTCAGACGAACATAACACTTCAGATTGCCACAGATGAA ::::::::::::::::::::::::::::::::	3810 3820 3830 38 GGTGACAAAGACCATATCGCGGTAGAACTCTATC ::::::::::::::::::::::::::::::::::::	3870 3880 3890 3900 3910 3920 CCGGCTCTCATCCAGCTTTTACAGTGTGGAGACAATCAAT
		3800 CTGTATAAGG : : : CATTA	3870 .ccggcrcrc?
3650 Slit AGTGTTTGCCTGGCT ::: :: :: 325 AGTCCTCT 1460	3720 3730 TTATCTTCAGATTCCTTCA(:.:::::	3790 3810 3820 3830 3840 3850 GACAGCGGAATCCTCTGTATAAGGGTGACAAAGACCATATCGCGGTAGAACTCTATCGGGGGCGTGTTC :::::::::::::::::::::::::	GACA
Slit AGTG ::: 325 AGT- 1460	Slit TTAT 325	Slit GACA 325	3860 Slit GTGCCAGCTAT :.:: 325 AA-CTTACTA- 1600

Fig. 2M-14

DG7EES11 C11G1

3990 CCCAAA	4060 IGCCAG	4130 CATCCG	4200 CCTGGC
3980 ATGGTGGGAACO .::::	4050 IGTAGGAGGCA'	4120 TTCCACGGCTG(:: TT	4190 AAACAGGCATTTTGC ::::: TTTTAATCATTTT
3970 TCTTTGTCCGTGG; :.:::: -CAATGTC	4040 TCCACTCTA	4110 GGAACCAGCTT : :::: 'GCTAGCTT 1730	4180 CGATGCAAA(
3960 AGTCTCTTTT :: CAAT	4030 ATTTTGACTC :.::: AAGTTGA	4100 TGGGCAGAACGG:::::: TTGACATTTTG- 1720	4170 CAGAAGGTGC ::: GTG-
3950 CTTGGATCAG	4020 4030 FCCACTCTGAATTTTGA ::::::::::::::::::::::::::::::::::::	4090 3CCAGGCCCC	4160 SCAGGACTTC
3940 ACTACTTGCC ::::::	4010 TCAAAGCAG:	4080 CATCTCTGCC:::	4150 CAGTGAGCTG
3930 3940 3950 3960 3970 3980 3990 Slit CTTCCACATTGTGCATCTTGGATCAGAGTCTCTTTGTCCGTGGATGGTGGGAACCCCAAA ::::: ::::::::::::::::::::::::	4000 4010 4020 4030 4040 4050 4060 lit ATCATCACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTCTATGTAGGAGGCATGCCAG :::::::::::::::::::::::::::::::::	4070 4080 4090 4100 4110 4120 4130 Slit GGAAGAGTAACGTGGCATCTCTGCGCCAGGCCCCTGGGCAACGGAACCAGCTTCCACGGCTGCATCCG :::::::::::::::::::::::::::::::::::	4140 4150 4160 4170 4180 4190 4200 Slit GAACCTTTACATCAACAGTGAGCTGCAGAACGTGCCGATGCAAACAGGCATTTTGCCTGGC ::::::::::::::::::::::::::::
32.	Slit 325 167	S1.	S1.

Fig. 2M-15

ODYKETT NITEDI

Fig. 2M-16

TOPECT LINEAPORT

Fig. 2M-17

noremil citagri

4830 AAAAGGTTG :.::. ATATAATTA	4900 \AAATAC ::: FAA	
4820 4830 IGTCTTTGGAAAAGGTTG ::: :::::.	4850 4860 4870 4880 4890 4 ATGTGGGACTAATGAATGCTTCATAGTGGAAATATTTGAAATATTTGTAAAA :: ::::::::::::::::::::::::::::	
4810 CGGCAGCTCJ	4880 AAATATTTG? . ::.::. .GCATTATTA?	4950 GCATTTG ::
0 4800 CCTAAACACACTCC ::: :: AAACCTC-	4870 4880 4890 CTTCATAGTGGAAATATTTGAAATATATT ::::::::::::::::::::::::::::::::::	4920 4930 4940 4950 TTTATTATGAGACTTTTTTTTGCATTTGGATTTTTTTTTT
4790 GTGTGTCCTAA :: AA 2060	4860 TRATGAATGC::::::::: ATAATGAATT? 2100	4910 4920 4930 4 GACTTATTTTATTAGAGAATAAAGACTTT :::.:.::::::: TAAAAAAAAAAAAAAAAAGGGCG
4780 CTGTACGAGGT ::: CTG	4850 CATGTGGGAC :: TGGAAATP	4920 TTTTATTATC :.:
4770 4780 4830 4830 4830 4830 4830 4830 4830 48	4840 4850 4860 4870 4880 4890 4900 Slit TATACTTCTTGACCATGTGGGACTAATGAATGCTTCATAGTGGAAATATTTGAAATATTGTAAAATAC :::::::::::::::::::::::::::::::	4910 Slit AGAACAGACTTATT :: 325TAAA 2140
Slit 325	slit 325	Slit 325

Fig. 2M-18

158 79 20 40 9 80 234 294 354 414 474 100 534 120 SCAGCTCTGGGGGAGCTCGGAGCTCCCGATCACGGCTTCTTGGGGGTAGCTACGGCTGGGGTGTGTAGAACGGGGCCGGG GAG CAG GCTGGGGCTGGGTCCCCTAGTGGAGCCCAAGTGCGAGAGGCAAGAACTCTGCAGCTTCCTGCCTTCTGGGTCAGTTCC CTA GTA 300 GCG Ц > 回 ď Ø ď TTATTCAAGTCTGCAGCCGCCTCCCAGGGAGATCTCGGTGGAACTTCAGAAACGCTGGGCAGTCTGCCTTTCAACC CTG GTG CAG GGC GAG CTA Ц 口 > Ø Ö 口 CTG GAC GIG GTG TCC GAA Д > ഗ 口 > CTG GAC CAG CGC GCA TCA Ω Ø ഷ ď വ GGC AAC CIG ACC GGG GCC Ц ⊱ U ď Ö Z CGC TGG GAG GGC CGA GAG 闰 വ U 口 ഷ 3 GCC TAC CTG CTG TAC GAA ᆸ ≻₁ ᆸ ď × 回 GAG TTC GGC GCT CIC GAG ᆸ 臼 Ö ď 团 [I] GTG CCT GCG CCG GGT IGC U ᠐ Ø Д > വ CCC GAC GGG GCG AGC TCA Д ഗ r Ø Ω Ø CGC GTG TGG PCCC CTG GTG ᆸ > > U Z GAC ATG JGC AAA CGG CAT ر ک × Д ഷ Σ GCA CTG GAG CGG GCT CTT Ц Ы വ Þ ø 团 gcc GAC GGG CCC GGC TGG Д Ċ Д ט Þ ⋈ CAG TAC AAC GGA ACA GCA Ø × ტ ď z H CIG GTG AAA CGC GGC TTT 口 Ö > × R Ĺτι ICC TCC CTG CAA CCA TCA Ы Ø വ Д ഗ ß CAC CCC CIG GTG GGG GCA ט Д CCC Γ GTG CCG GTG CTG > > ᆸ ATG CCG CTG T ACT Q CAA CTA 口 Ц

ig. 3A

654 220 894 160 180 200 834 774 954 1014 280 R CGG E S AGC R CGC P CCA LCTC H Y TAC L P S TCC Q CAG I ATC W TGG S TCA A GCA A GCC H GGG CAC L CTG P Ŋ H P CCA K AAG P AAT ACC N AAT P CCT z ⊣ S AGC GGT S AGC F TTC M ATG I ATC Q CAA P CCC g GGC G GGC S TCC S AGC AGG D GAC PCCT Q CAG α E GAG N AAT R CGT CGC CAA E GAA ი მვვ ഷ L CTG S AGC D GAC A GCT S AGC LCTT E GAA S TCA T ACA S TCC Q CAG CCT G GGC S AGT Д ACG P C TGC GTG LCTC R AGG Γ E > AGC S TCC T ACA L TIG L GTG C TGC 口 > V GTC P GCC GGC CAC GGC K AAG s TCT ď Ŋ \mathbf{H} \mathcal{O} R CGG A GCA K AAA TTC CCT GCC L CTC PCCT ď ഥ Д V GTG L CTG V GTC M ATG GAG CAT E GAG ഥ Ή TACC GAG L TCA A GCT S TCC GCT Ø 团 വ GTG CTG ACG ACC G GGA GTG CTT> Ы H Н \gt 口 D GAC G GGC GTG $_{
m TTC}$ α > \gt 团 CAG $\overline{\mathbf{W}}$ GCC TCC R AGA TGT Ø ø \mathcal{O} ഗ g GGC T ACC а 9 R CGG GCT GTG ACT ø > ⊱ H L E GAG V GTG Γ I ATT S TCT

Fig. 3B

300 320 360 380 400 420 E GAG G GGG L TTG CAG AGG BCC CCC വ് Д T ACT CIC GCC N AAT s TCT CGG AGA GAG ĸ 口 D GAC GAC S AGC GCA AAG ATC CTG GAA Ø О × ᆸ 团 G GGG V GTC GAA GCC CGC TCC GGG S AGT 口 വ ß r I ATC D GAT Q CAG AAC H CAT CGG GTA ATG 엄 > \mathbf{z} Σ VGTG C TGC GTG GAG GTG P CAT AGT 出 臼 ഗ \gt V GTC D GAC GGT TAC GAG R CGA AGG $\boldsymbol{\sigma}$ ഷ 闰 ß V GTA $^{
m Y}$ L CTT GTG CGA ACC GAG TGC > α Н \mathbf{c} 団 GTG CTG G GGG I ATC VGTT TCC CCG AGC ഗ Ц ഗ Д ACC GTG S AGT G GGC D GAT ATG CAG AGT > ⊢ Ø വ GIG CIC CTG AAC S AGC AGC > \gt Ц വ Z GAC GTG TCG AGG Γ H T ACT GAG > വ 臼 Д 足 V GTC AAG E GAG A GCC GIG GAG CCC P CCT > ഠ Д ĸ Q CAG GAG GAC CIC G GGG GTG T ACT > Ы വ 闰 Ω TACC S TCT GIG GTG TAT ACG AGT വ \vdash GAT GAT CTA GTG AAA CAC ᄓ Ы Ω \bowtie 出 Д AGG CTG CAG PCCA CAT P CCT ᆸ α Ω \circ Ή CAC P T ACA CTT 出 П ⊣ ß Ŋ \gt S TCC CAG C TGC CAT GGC F TTT Ø Σ 出 r CTG E GAG F FTTC CAG G GGC K AAG Ц Ø

Fig. 3C

460	CTG 1614	480	1674	200	1734	511	1767
Ы	CIG	Ø	CAG	ტ	GGC		
	GAA	X	AAA	z	AAT		
H	ACT	н		ტ	CGC		
Ø	CAG	ט	GGC	⊣	ACG		
Ħ	ACA	ы	GAA	Д	CCC		
	GAA	Q	GAT	×	AAG		
Н	ATA	Ø	CAG	Ą	BCC		
囝	GAG	О	GAT	ద	CGG		
ద	AGG		GAA	Ц	CTA		
>	GTG	闰	GAG	⊢	ACC	*	TGA
⊢	ACG	田	GAG	ტ	999	>	GIC
⊢	ACC		GAG		AAT	Ы	CIG
ᄓ	CIG	А	GCC	団	GAG	H	CAC
⊱	ACG	ద	CGG	Ø	CAG	ט	GGA
ഗ	ICC	ტ	999	>	GTT	ద	CGG
×	TAC	യ	TCT	Гц	TIT	ט	GGG
വ	AGT		GGC	H	CAT	Z	AAT
ద	CGC	Д	CCA	Z	AAC	Н	ATC
ტ	GGC	ഗ	TCT	Σ	ATG		TAC
田	GAG	Ы	CTG	Ø	GCC	н	ATC

2004 2083 2320 2399 2478 2557 2162 2241 1925 CCAGGCCTGCCTCCCTTCCCTAGGCCTGGCTCCTTCTGTTGACATGGGAGATTTTAGCTCATCTTGGGGGCCTCCTTA CTGACTGTGTGTGTGTGGAGGGGTGACTGTCCGTGGAGGGGTGACTGTGTCCGTGGTGTGTTATTATGCTGTCATATTATCAG GTTACAGAAGCCCTCTGCCCTCTGGTGGCCTCTGGGCCTGCTGCATGTACATATTTTCTGTAAATATACATGCGCCGGG CATGTGGCTGTGTGTGACCTCTGCCTGAAAAGCAGGTATTTTCTCAGACCCCAGAGCAGTATTAATGATGCAGAGGTT GGAGGAGAGAGGTGGAGACTGTGGCTCAGACCCAGGTGTGCGGGCATAGCTGGAGCTGGAATCTGCCTCCGGTGTGAGG **ITTTATTTATTTTTTTTTTTTTTTTTTTTAGAGATGGAGTCTCACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGC** GAACCTGTCTCCTACCACTTCGGAGCCATGGGGGCAAGTGTGAAGCAGCCAGTCCCTGGGTCAGCCAGAGGCTTGAACT

Fig. 31

2873 3426 3505 2952 3031 3110 3189 3268 3347 TCTGGCCTAAGGGAGAGGCTCCCATCCTTCGTTCCCCAGCCAAGCCTAGGACTTCGAATGTGGAGCCTGAAGATCTAAGA TGGGTTTTGGATCACTAATTCAAGGCTCTTCTGGATGTTTCTCTGGGTTGGGGCTGGAGTTCAATGAGGTTTATTTTA TCAAGCAATCCTCCTGCCTCAGCCTCCCTAGTAGCTGGGACTTTAAGTGTACACCACTGTGCCTGCTTTGAATCCTTTA CGAAGAGAAAAAAAAATTAAAGAAAGCCTTTAGATTTTATCCAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCCT GGCACCTGAGAGCTGGTAGAGTCTGAAATTAGGGATGTGAGCCTCGTGGTTACTGAGTAAGGTAAAATTGCATCCACCA GCAGTGATTATAGACCGAGAGAGTAGGAGTTGAGGTGAGGTGAAGGAGGTGCTGGGGGGTGAGAATGTCGCCTTTCCCCC GCTGGCCCACCCAGATACACTCAGCCAGAATACCTAGATTTAGTACCCAAACTCTTCTTAGTCTGAAATCTGCTGGATT

Fig. 3E

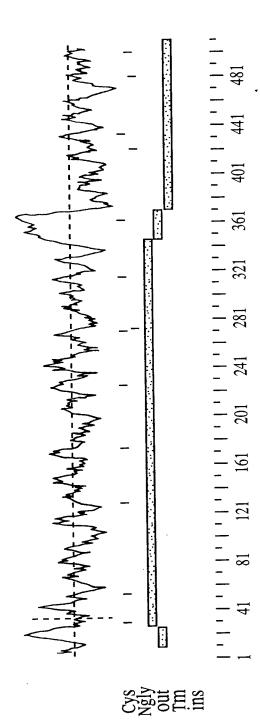


FIG. 3F

DS7GST1 D11001

118 59 178 79 238 99 119 358 418 159 139 TACC A GCT A GCT GAT TCT CTA Д വ ഗ CTT GGA L CTG GAT GAC Ċ П О Ω ACC GIG TIC GAA CGG AGG GTG CCA > ப ഥ ഷ Д ഷ GIC \mathtt{TGT} S TCC AGA ACA CCC TCA Q CAG ഷ Н ഗ ACT GIG GGC TGG TTTCC AAG > U ¥ Z ഥ ഗ GCT CTG CAC I ATT AAC GGC GGG TIC H 王 ᠐ ט z ഥ $_{
m ICI}$ ഗ TAC CCA CIC CAC TIG GAG TCT工 \succ 니 闰 ß Д CGC CAG I ATC W TGG TCA ACT AAT GAC Ø ഗ О H z ICC ഗ GGG CAC CCC GAC S AGC Γ GAA ᠐ Д 闰 Ή Д CAC AAT GTC ACC AAT CCTGGG Q CAG H Д Ü > z Z AAG × ATG I ATC P CCC CAA CCC GAT CAT Ω Ø വ 口 Σ AGC AGG GAC Q CAG GTG IGC GAC വ U Ω ద О > $_{\rm LCC}$ വ CGC CAA GAA GGG CGA GIC GCA Ø O 闰 ᠐ ሥ > CGT ద AGC TAC GAC CTT CTT GAA GTA Ы О ഗ Ы 口 > × AGC ഗ CCI CAG ATC GTTGGC AGT GGG Ø Д Ŋ ტ Н > ß $_{\rm LCC}$ GTG GGC GAT CIC AGG CTG AGT П Ω α Ц Ŋ ტ ACG AGC TIG CCC GTG CTG GTG TGC ט Ŋ > ᄓ Д ACA CAC GGC AAG CTG ACT ᠐ × 耳 വ GGC gccCTC GAG CCT CCT 闰 T ACT Q CAG E GAG M ATG GGG CAT 工 U ט

Fig. 3G

179	538	199	9	219	658	239	718	259	778	279	838
>	GTG	×	AAA	H	CAC	₽	ACG	臼	GAG	ט	GGG
Ц	CTG	Ø	CAG	H	CAT	⊢	ACC	凶	GAG	z	AAT
ᆸ	CTT	E	ACC	ഗ	ICC	ᆸ	CTG	Ą	GCC	臼	GAG
ט	IGC	Σ	ATG	H	CAT	₽	ACG	ద	CCC	Ø	CAG
ഥ	$_{ m LLC}$	Ø	CAG	П	CIG	വ	ICC	ט	999	\triangleright	${ m GTT}$
ц	${ m TTG}$	Ø	CAG	ద	AGG	∀	TAC	യ	TCT	됴	${ m LLL}$
П	CIC	Ą	BCC	ద	CGG	ഗ	AGT	ტ	GGC	Ħ	CAT
Ø	GCA	×	AAG	Н	ATC	ద	CGC	വ	CCA	N	AAC
Ą	GCC	ద	CGC	വ	ICC	ט	GGC	ഗ	TCT	Σ	ATG
Н	ATC	ద	CGG	Z	AAC	田	GAG	Ы	CIG	A	GCC
>	GTG	H	CAT	田	GAG	Д	CCC	П	CIG	Ø	CAG
ტ	GGI	×	TAC	ద	AGG	闰	GAG	Ш	GAA	×	AAA
>	GTG	ద	CGA	⊢	ACC	Щ	GAA	H	ACT	Н	ATC
>	GTG	Ø	ICC	Ц	CIG	വ	AGT	Ø	CAG	ט	GGC
>	GTG	Σ	ATG	⊢	ACC	Ø	CAG	⊢	ACA	田	GAA
>	GTG	ᄓ	CIC	П	CIG	ഗ	AGC	臼	GAA	Д	GAT
യ	TCG	>	GTG	Œ	GAG	ద	AGG	Н	ATA	Ø	CAG
Ø	BCC	>	GTG	臼	GAG	д	CCC	臼	GAG	Ω	GAT
വ	TCA	>	GTG	臼	GAG	Ω	GAC	ద	AGG	臼	GAA
>	GTG	>	GTG	≯	TAT	⊣	ACG	>	GTG	臼	GAG

V GTC L H GGA R CGG ი მემ N AAT I ATC Y TAC I ATC g GGC N AAT g GGC T ACG PCCC K AAG A GCC R CGG L CTA

299 898 300

* TGA

TACC

Fig. 3H

NOTEERLA DIAGOLA

CCCAGGCCTGCCTCCCTTCCCTAGGCCTCCTTCTGTTGACATGGGAGATTTTAGCTCATCTTGGGGGCCTCTTA	980
AACACCCCCATTTCTTGCGGAAGATGCTCCCCATCCCACTGACTG	1059
GAGGGCTCCACCAATTGAGTCTCTCCCACCATGCATGCAGGTCACTGTGTGTG	1138
CTGACTGTGTGTGTGTGGAGGGGTGACTGTCCGTGGAGGGGTGACTGTGTCTCGTGTGTGT	1217
AGTCAAGTGAACTGTGGTGTATGTGCCACGGGATTTGAGTGGTTGCGTGGGCCAACACTGTCAGGGTTTGGCGTGTGTGT	1296
CATGTGGCTGTGTGTGTCTCTGCCTGAAAAAGCAGGTATTTTCTCAGACCCCAGAGCAGTATTAATGATGCAGAGGTT	1375
GGAGGAGAGAGGTGGAGACTGTGGCTCAGACCCAGGTGTGCGGGCATAGCTGGAGCTGGAATCTGCCTCCGGTGTGAGG	1454
GAACCTGTCTCCTACCACTTCGGAGCCATGGGGGCAAGTGTGAAGCAGCCAGTCCCTGGGTCAGCCAGAGGCTTGAACT	1533
GTTACAGAAGCCCTCTGCCCTCTGGTGGCCTCTGGGCCTGCTGCATGTACATATTTCTGTAAATATACATGCGCGGG	1612
AGCTTCTTGCAGGAATACTGCTCCGAATCACTTTTTAATTTTTTTT	1691
TTTTATTTTTTTTTTTTTTTTTTTTTTTAGAGATGGAGTCTCACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGC	1770
TCAAGCAATCCTCCTGCCTCAGCCTCCCTAGTAGCTGGACTTTAAGTGTACACCACTGTGCCTGCTTTGAATCCTTTA	1849
CGAAGAGAAAAAAAAATTAAAGAAAGCCTTTAGATTTTATCCAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCCT	1928
CCAACACCAGGGGGTTAATTCCTGTGATTGTGAAAGGGGCTACTTCCAAGGCCATCTTCATGCAGGCAG	2007
GGCACCTGAGAGCTGGTAGAGTCTGAAATTAGGGATGTGAGCCTGGTGACAAGGGCTCCTGTTCAATAGTGGTGTTGGG	2086
GAGAGAGAGAGCAGTGATTATAGACCGAGAGAGTAGGAGTTGAGGTGAGGTGAAGGAGGTGCTGGGGGGTGAGAATGTCG	2165
CCTITCCCCCTGGGTTTTGGATCACTAATTCAAGGCTCTTCTGGATGTTTCTCTGGGTTGGGCTGGAGTTCAATGAGG	2244
TTTATTTTAGCTGGCCCACCCAGATACACTCAGCCAGAATACCTAGATTTAGTACCCAAACTCTTCTTAGTCTGAAAT	2323
CTGCTGGATTTCTGGCCTAAGGGAGAGGCTCCCATCCTTCGTTCCCCAGCCAG	2402
AGATCTAAGATCCTAACATGTACATTTTATGTAAATATGTGCATATTTGTACATAAAATGATATTCTGTTTTTAAATAA	2481
ACAGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2510

Fig. 31

1	RV 70	1	QAR 140		HL ::	FHL 210	PSY ::: PSY 280
! ! !	QVAWA	 	AGSFQ 1	20	VTSEF	VTSEF 2	90 30PPP 30PPP 30PPP
	YRGDSGEQVG(60		EYECRVSTFP/ 130	10	-KGTTSSRSFKHSRSAAVTSEFHL	RSFKHSRSAA) 200	80 .EGAMLKCLSE ::::::::: EGAMLKCLSE
	7LGQDAKLPCF 50		LLRNAVQADEG 120		KGTTSS	NDTEVKGTTSS	70 LEDQNLWHIGR ::::::::: LEDQNLWHIGR 260
	ELETSDVVTVV 40		PPRNPLDGSVI 110			AEGSPAPSVTV 180	0 80 90 THILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPP :::::::::::::::::::::::::::::::::::
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV 20 30 40 50 60 70	 	GLHVSPAYEGRVEQPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQAR 90 100 110 120 130			PALEEGQGLTLAASCTAEGSPAPSVTWDTEVKGTTSSRSFKHSRSAAVTSEFHL 160 170 180 190 200	0 HPGLLQDQRITHILHV ::::::::::::: HPGLLQDQRITHILHV 230 240
	PEAWLLLLLL 20	 	LHSKYGLHVS 90		 		40 .TCVVSHPGLL :::::::::: .TCVVSHPGLL
	MPLSLGAEMWGPEAWL 10		DAGEGAQELALLHSKY 80			T364 LRLRVLVPPLPSLNPG 150	30 40 50 90 ALT VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY ::::::::::::::::::::::::::::::::::
ALT	T364	ALT	T364		ALT	T364	ALT T364

Fig. 3.1

	100		110	120	130	140	150	160
ALT T364	NWTRLDGPLPSGVRV:::::::::::::::::::::::::::::::::::	PLPSGVRV ::::::: PLPSGVRV 290	VDGDTLGFPP ::::::::: VDGDTLGFPP 300	LTTEHSGIY :::::::: LTTEHSGIY 310	VCHVSNEFS ::::::::: VCHVSNEFS 320	SRDSQVTVDVI ::::::::::: SRDSQVTVDVI 330	ALT NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLADPQEDSGKQVDLVSAS :::::::::::::::::::::::::::::::::::)LVSAS :::::)LVSAS
ALT T364	170 T VVVVGVIAALLFCLL::::::::::::::::::::::::::::::::	AALLFCL) AALLFCL) AALLFCL) 360	180 LVVVVVLMSR ::::::::: LVVVVVLMSR 370	190 YHRRKAQQM' ::::::::: YHRRKAQQM' 380	200 TQKYEEELT :::::::: TQKYEEELT 390	170 180 200 210 220 ALT VVVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ- ::::::::::::::::::::::::::::::::::::	170 180 200 210 220 ALT VVVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ :::::::::::::::::::::::::::::::	SVGLR
ALT	 	; ; ; ; ;	230 SEEPEGR	240 SYSTLTTVR	250 BIETQTELL	260 SPGSGRAEEER	230 240 250 260 270 SEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN	FVQEN
T364	4 AEGHPDSI 420	KDNSSC	:::::: SVMSEEPEGR 440	::::::: SYSTLTTVR3 450	::::::: EIETQTELL 460	:::::::: SPGSGRAEEEE 470	::::::::::::::::::::::::::::::::::::::	::::: FVQEN
•	280	290						
ALT	ALT GTLRAKPTGNGIYINGRGHLV	rgng i Y i i	NGRGHLV					
T364	T364 GTLRAKPTGNGIYINGRGHLV	GNGIYI!	:::::: NGRGHLV					
4.	490	200	510					

Fig. 3K

DEFECT LIMES

55 CTTAATGTTGGAAGTCTCTTAGTCCTATGAGAGTGTGTAGCAGTTTGTCCCTGAG CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTTAGGGAGAGAGGGTACAAAAGGTTCCTGGACCTTCTC

15 198 35 TGG TIC ſΞι ⋈ GGC TGC U U AGA GCT ď 民 AAA AGT \bowtie ഗ GAG CIC Н 闰 ACA CIC Н Н AGT GCA Ø വ CAA ATT O Н CCTICC Д Ø CAA ATT Ø Н CAG GGG Ø U GAG GCT ď Ы GTG CAA Ø > ATG TCT Σ ഗ ATG TGG Σ ⋈ AACACAGGGAGCCTGCATA CIC П AGA α CTG 口 TCC വ П

52 318 TCT ø Ø CTG Ы വ AGG 民 AAA × X GGC Ö ⊱ ACT Н Ċ GAA 团 闰 GGT U വ TAT × ᅜ ACA U ⊣ TTTᇿ ⊱ CAT 耳 ᆸ TAC × വ ACT ĘΗ വ GTA > 田 GTA > × TGT U വ AGC 呂 വ GTG Ц TTG ATT 口 Н

378 438 GCC AGT വ ICC CCA വ GTG ATT Н AAG TIC ഥ ACA TAC × GGG IGC U GAA AGT വ AGT TCC ß TIC GGT Ö IGC TTT ഥ ACC TCA ഗ CIC AAG × AGT TGG Z TCA TCT ß CAT GCT Ø TAT CCA Д TCA TGC Ŋ CAC TGT U CTA GGA ט TGG GAA ≊

115 498 GTT \gt TTG Ы CAT 口 GCA ď GGA Ċ ATG Σ GAG 闰 GTT > $_{\mathrm{IGT}}$ U AAC Z CAG Ø GAG 团 AGT ഗ AAG × TCT വ TGG ⋈ GTT > AAG × GAG 凶 GAA 闰

TCT Ŋ TTT ഥ TCA വ GAG 臼 AAT Z CTG Ы CAG Ø CAG Ø GIC > ATT Н TTCഥ AAT Z CAG Ø GAG 口 GCA ď GAA 団 ACA Н AAC z TIC GTG >

Fig. 4A

155	175	195	210
618	678	738	
T	O	E	
ACA	CAA	GAA	
K AAG	EGAG	C TGT	
D	A	I	
GAT	GCA	ATC	
I	S	V	
ATT	TCT	GTT	
W	H	D	
TGG	CAT	GAT	
Q	N	N	*
CAA	AAT	AAT	TGA
W	r	W	L
	CCC	TGG	CTA
N	E	G	Y
AAT	GAG	GGC	TAC
N	G	W	I
AAT	GGT		ATT
N	L	G	K
AAT	CTA	GGA	AAG
GGT	H	T ACA	N AAT
Q	M	P	M
CAA		CCT	ATG
PCCA	F	K	E
	TTT	AAA	GAG
D	R	W	C
GAC	AGA	TGG	TGT
S	V	F	I
TCA	GTC	TTC	ATA
L	N	V	S
	AAT	GTC	TCA
G	K	I	N
GGG	AAA	ATA	AAT
L	E	S	R
CTG		TCA	AGG
F	Y	A	R
TTT	TAT	GCT	AGA
Y	P	C	T
TAT	CCT	TGT	ACT

1099 862 1020 1336 1415 941 1257 1494 1573 CTITIAATCAATCTTCTCGTTTTCCTTTTTCCATTAATGATAGAATGCACCTTCCTCTTTGTTCCATTCTTTCACTT GTTATTCATTTTTTTTTCTTCACACTTCATTACACAAATATTTATTTTTCAGAGACTGTACTATTTTGTTAG AAGCATTTCTTGTTACCCAAATCTAACCTATTCCTGAAAATATGATGGTTAGCAAAGTTTGAGATAACTAGAGCCTGTA TACCAAAATGGTCATTAATCTGTATCCACAAAGGATTTCTGCATTACATACTTTAAAACAAATTACCTAATTATTTAGT GTAGAAGCTTAATTGGAAAGAAGAAGAATTACTGACGTAATTTTTTTCCCTGACGTCTTTAAAATTGAACCCTATCAT GAAATGATAATTTCTTCCTGAATTTACACATAATCCTTATGTTATAGAGGTTCACAGAAATGGAAAGATACCTGTTTCC

3114	THE STATE OF THE PARABABABABABABABABABABABABABABABABABABA
3074	ACAAAGATTTCACACATGAATACCTATGTAACAAATCTCCATGTTCTACACATATACCCCAGAACTTAAAGTATAAA
2995	AACTTTGCCCTAAAAGTTAAGACATATTCTGAGAATCATAATAGTCACATGATTTCTGATGCTATCTGCTGTTAATA
2916	TTAAATTATTGAAGTCTGAGTTTTCAAAAGTGATTTTTTCCCACAAAGGTGCCAACACTTAAGCTAGAGCTTTCAGTGTT
2837	ATGAATCATTAAGACAGTAATTAGGAGTTCACAAATTTAAAACATTTCACGTAATTTTAAAATTATTGTCTTCAATAATT
2758	AAAACTCCATGGTTTACAGGCATGTCATATTGAAAATAAAGCTGCAATAGCTTTTTTATACAATTATGCTCTCTCAAGAAA
2679	ACAAAATGTGTAACAAGAAACTAATGACCTTTCTAAAATCAAACATTCAAATTATCTACAATGTCTATTTACAAACAGGG
2600	ACAACTTTTATTAGAAAAGTTATACATAACACAGCATCAACTATTTTCAAGAACCCAATAAGCAACAAAAACCAGACTA
2521	TATATGGTTCTAAATCTATCTTACTAGGTGGTTTCCATTTCCTCTGCTCCAAAATATTTTTTTT
2442	AAATTTTAAAAAATCCCAATGGCAATCACCTTTTAGGTTAAAAATTTAATCCATTTACATTTGTGACAATTCGACATA
2363	TGCTGTAAAATTTTTTTTCCATCTTCTATTTTTGACCATTTTTTATTCCACATGTGCTCTTAATAAGTAGCATATAGTT
2284	TTCTTTAAATTTTAGTAATGCCTTTTGGCTTTTAATTTTTCTCCTGATATTAAAATAGATACAGTAACTTTCATTATGTTAG
2205	AGCCATGATGAGGTATATACAATGTTATAATTATTACTTGTACATGGCAAATTAATT
2126	GGCACAACAATTTTTAAATTTAACTATTTTGGATATTTGGATATTTAAAGCTTCTTATAGAAAGAGATACCTGTATATTTA
2047	ACTCATGAGCAACTTGAATAGTTGTAACTGTGATGCATATGTAGATTCTAACACATTTTTCCCCCTTGAATAGAAATTT
1968	TGGCAGTAGGAGCCTATAAAGGGATAAGCAATTGGGAAAGGATTGGGAAGTTGGTAGTACTGAACATCTTCTCACCTGG
1889	TTGCACTGAAAATACCATAATATAAAGAAGAATCCCATCATCCAAATTGAGCCTATATTGATTG
1810	GCATATTAAACTTATTGGTGGGCATGACTATATGCAACAGTTGCATGATATGATACAAATTATGTTATTTTTTTT

Fig. 4C

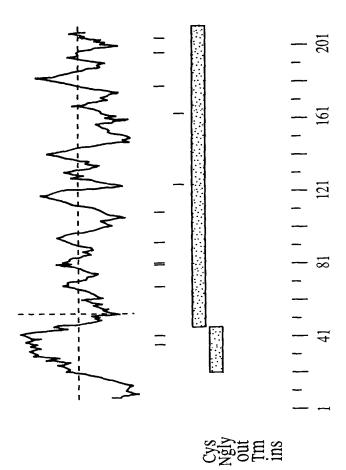


FIG. 4C

158 GAACTCTGGCCTCTTTGACAGAAGCCAGGTCCCTGAGTCGTATTTTGGAGACAGATGCAAGAAACCCCTGACCTTCTGA

16 36 76 401 96 221 116 281 341 461 521 Γ S AGC CAC TGG AAG GIG TAC > Ξ × ⋈ T ACC A GCG CTT ATG T ACC GTG TCT > Н Ø Σ TGG I ATT GAA AAA CTGTCT Ц ഗ × Jgc FTTC TAT GAA ATT CAT TCA Н 耳 \succ ഥ GIC TGT CTA CIC GAG TCA GCT 口 > ر ک ø П ഗ GGA ACC AGA GTG TAC GGG ᠐ × ы ĸ G z \gt AAG AGA AGT ATG IGC ATG CIG ပ Н × ഗ Σ മ്പ Σ GGG $rac{ ext{L}}{ ext{TTG}}$ AGC CAG CAG ACT AGT G ഗ Ø Q ഗ ⊣ CAA L CIC CCC GGG ICC GTT CAG > Ø Ø r S Ы ICC $_{
m LTA}$ CAG GAA GGC TGT ACC ပ U ഗ Ø ഥ ATC M ATG CAA AAC GAC AGT TTTO Ω ഗ Гщ Z Н AGA ATG ICC TIC CAG TTCTCA œ ഗ Ø ഗ GAA I ATT GAG AAT ATT AAG C × Ы 口 Z Н CAG GIG ACC $^{
m TGG}$ CAG AGT > O Ø 3 ഗ Ŀ CAC ACC A GCT L CTC GAG CAA 工 H O ATG GCG GCT TAC AGC AGT AAT Ø K ഗ Σ z വ ACATACACCTCAACA S TCA ACT ICC CCA IGG GAA Д ഥ 3 ⊣ S TGG GIG CAT TGC TIC ACT ပ 耳 ш L CTC GTG TAC IGC AAC AAT Ö > \succ z AGA ACA GAG Γ GT GGA G Еч

Fig. 4E

DSTECTIOTION:

K V AAG GTP	G	TTC CTG GGT CTT TCG GAT CCC
T 5	GGT TCT GGC ACC CCC ATG	GGC ACC
		F Q * TTT CAA TAG
lGT.	TGGGGCTGGGAATGATGT	TTTACTGGAATCCTTCGAAATGGGGCTGGGAATGATGTTTTCTGTGATAGTAAACACACAATTCAATATGTGAAATGAANA AGATTACCTATGAATGCCTGTTATTCTTAATA

Fig. 4F

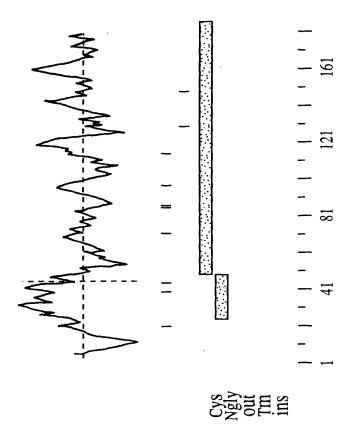


FIG. 46

70 :: EG	卢 년	> · Fi
7 CFSE	ESYF .:::	MNKI
HSSLT(::::: HSSLT(60	130 QQLNES :::::: QQLNES 130	200 ICETRRNSICEMNKIY : ::: 170
60 :::: ::::	EIVO E::: FITO	2 ETRRI : -TPMI
KRLSE .::: RRLYE O	D EAEON ::::: EAEON O	O NDVIC
50 GETGKI 	120 VFNTEZ : . : : : : : : : : : : : : : : : : : :	190 'GWGWN] : :
YHFTY : - : · YQFIM	SAHLV ::::: SAHLV	FWKPTGW : .: KMSGS 160
40 SCVVT SCVVT 40	110 UCVEMC I::::: UCVQMC	180 ASIV]
CFIVE	KSEQN :::3 TSEQN	170 180 190 SEPNHSAEQCASIVFWKPTGWGWI : : : : : : : : : : : : : : : : : :
20 50 70 70 70 50 60 70 50 60 70 20 10 10 10 10 10 10 10 10 10 10 10 10 10	90 100 110 120 130 KSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL ::::::::::::::::::::::::::::::::::::	170 GEPNH9 150
AGISI ::::	TISSE .::. LISTK	REWHL
20 RLWSV7 ::::: RLWSA7	90 SSCYI	160 EKNVI
Z WLSLR : · :: W-TLR	WKSFG ::::: WKSFG	DKTPY
) TEKRGI KGVC-1	80 *::::: ******************************	150 NWQWI : .N
10 QPQSTE : . : . QSQGKG	WG(::: KMWG(QGNNN KVMAN
1 MMQEQQPQS :.::.:.: MVQERQSQG	TKVPA:.: TMVSEKN 70	140 GLSDPQ ::::: GLSDPK 140
10 human MMQEQQPQSTEKRGW ::::::::: murine MVQERQSQGKGVC-W	80 100 110 120 130 human TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL ::::::::::::::::::::::::::::::::::::	140 150 200 human GLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIY ::::::::::::::::::::::::::::::::::::
hı mui	hı	hı muı

human L

murine Q

Fig. 4H

COPERTION TOOL

70 1GG 31G	140 ATA 	210 GGG ::: GGG	ACT:
STCTG' ::::: STCAGG	TTTAC:::: TTTAT: 130	3TGAA(:::: 3TGAA(200	270 TTGCT/ :::: TTGCT/ 270
60 TCTGC::::	130 ACCAT1 :::::: ACCAA1	200 CTTCAC ::::::	CCAGI
30 40 50 60 70 ACAGAGAAAAGAGCTGGTTGTCCCTGAGACTCTGGTCTGTGG ::::::::::::::::::::::::::	80 90 100 110 120 130 140 CTGGGATTTCCATTGCACTCCTCAGTGCTTGCTTCATTGTGAGCTGTGTAGTAACTTACCATTTTACATA ::::::::::::::::::::	160 170 180 200 210 AAAGGCTGTCTGAACTACATTCATTCAAGTCTCACCTGCTTCAGTGAAGGG .::::::::::::::::::::::::::::::::	230 240 250 260 270 CCTGGGGATGTTGCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT :::::::::::::::::::::::::::::::::
50 TCCCT .:::	120 GTAGTA ::::: GTGGTG	190 GTCTCA ::::::	TCATT ::::: TCATT
3GTTG : : : 3CTGG 40	1 CTGTG ::::: CTGTG	1 TCAAG :: :: TCCAG	250 GGAAG :::: GGAAG
40 AGGCT(:: :: AGTCT	110 TGTGAG	180 TATCAT' ::::: TACCAT'	FTCTT(:::
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	17 TCATT(::::TCATT(18 CTCATA :.::: CACATA	230 240 TGGGGATGTTGCCCAGCTT :::::::::::::::::::::::::::::::::::
30 CAGAG <i>I</i> ::::: -AGGG <i>I</i>	10 TGCT1 TGTT1	0 TACAC::::	TIGCC
3 AGTAC	100 GTGCTT :::::	170 CTGAACT. ::::: ATGAACT' 160	230 GGGATG :::::: GGGATG 230
20 CCTCAA : :: TCCCA- 20	90 TCCTCA :::::	0 CTGTC ::.: CTATA	2 TGG ::: TGTGG
20 AGCAACCT .::: SACAATCC	GCACT ::: TTACT 880	160 AAAGGC .::::: GAAGAC	C AAAAA 20
SAGCA SABCA SAAAG	CCATT) rggca .:: cagta	CCAGC
10 20 ATGATGCAAGAGCAGCAACCTCAA ::::::::::::::::::::::::::::::	80 CTGGGATTTCCAT ::::::::::::: CTGTGATTTCCAT	150 TGGTGAAACTGGCA : : : : : GGACCAGCCCAGTA	220 ACAAAGGTGCCAGC ::::::: ACTATGGTGTCAGA 210
		150 160 200 210 human TGGTGAAACTGCAAAAGGCTGTCTGAACTACACTCATTCAATTCAAGTCTCACCTGCTTCAGTGAAGGG : : : : : : : : : : : : : : : : : :	
human murine	human murine	human urine	human murine
d m	h mu	d m	h m

Fig. 41

COPERTION OF THE

human murine	280 330 340 human TCATTTCCAGTGAAGGTTTGGTCTAAGAGTGAGCAGAACTGTGTTGAGATGGGAGCACATTTGGT :::::::::::::::::::::::::::::::	290 GAAGAGAAGGT .:.::::: AAGGAGAACTT 290	300 TTTGGTCTAAG: : ::: TCTGGAGCACC: 300	310 320 330 34 AGTGAGCAGAACTGTGTTGAGATGGGAGCACAT ::::::::::::::::::::::::::::::::::::	320 ACTGTGTTGA ::::::::	330 GATGGGAGCA(:::::::: GATGGGGGCT(330	340 ATTTGGT:::::ATCTGGT
human murine	350 360 400 410 TGTGTTCAACACAGAGCAGAGTTTCATTGTCCAGCAGCTGAATGAGTCATTTTCTTATTTTCTG ::::::::::::::::::::::::::::::::	360 CAGAAGCAGAG :.:::::: CTGAAGCGGAG	380 390 400 SAAGCAGAGAATTTCATTGTCCAGCAGCTGAATGAGTCAT ::::::::::::::::::::::::::::::::::	380 TTGTCCAGCA(: : : : : : : TCACCCAGCA(390 GCTGAATGAG' ::::::::: GCTGAATGAG' 390	400 ICATTTTCTTA ::::::::: ICACTTTCTTA 400	410 ATTTTCTG ::::: ACTTCCTG 410
human murine	420 430 440 450 460 470 480 GGGCTTTCAGACCCACAAGGTAATAATTGGCAATGGATTGATAAGACACCTTATGAGAAAATGTCA ::::::::::::::::::::::::::::::::::::	430 CCCACAAGGTP ::::::: TCC-CAAGGTP 430	0 440 450 CAAGGTAATAATTGGCAATGGATT :::::::::::::::::::::::::::::::	450 GCAATGGATT(::::::: GCAATGGATC(450	460 470 GATAAGACACCTTATGAG ::::::::::::: GATGATACTCCTTTCAGT 460 470	470 CTTATGAGAAA ::::: CTTTCAGTCAAA	480 AAAATGTCA ::::::: AAAATGTCA 480
human murine	490 500 510 520 530 540 550 GATTITGGCACCTAGGTGAGCCCAATCATTCTGCAGAGCAATGTGCTTCAATAGTCTTCTGGAAACCTAC :.:::::::::::::::::::::::::::::::::::	500 CTAGGTGAGCC : .:::: CCCCATGAACC 500	0 510 520 53 GTGAGCCCAATCATTCTGCAGAGCAATGTG .::::::::::::::::::::::::::::::::::	520 GCAGAGCAAT(: :::::: GAAGAGCGGT(520	530 5TGCTTCAAT: ::::::::::::::::::::::::::::::::::	540 AGTCTTCTGG/	550 MAACCTAC

Fig. 4.

DOPERLY DITOR

620	ATAAGATTTAC	
610	rgtgagatga <i>i</i>	
009	SAATTCAATAT	
290	AAACTAGAAG	
580	SAATGATGTTATCTGTGAAACTAGAAGGAATTCAATATGTGAGATGAATAAGA	
570	TGC	
260	AGGATGGGGC	
	human	

human CTA

murine --

murine ---

Fig. 4K

nareett natana

	10	20	30	40	50	09	70
mT405	mT405 MVQERQSQGKGVCW7	FLRIWSAAVI	SMLLLSTCFIA	ASCVVTYQF1	MDQPSRRLYE	ITLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGTM	EGTM
		•••	••	••••••			
Dectin	Dectin MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGTM	FLREWSAAVIS	SMLLLSTCF17	ASCVVTYQFI	IMDQPSRRLYE	LHTYHSSLTCFS	EGTM
	10	20	30	40	50	09	70
	C	o	100	110	120	130	140
	0	0	00	7	170) 1) † H
mT405	mT405 VSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFLGL	SFGSSCYLIST	TKENFWSTSE(ZNCVQMGAHI	VVINTEAEQN	FITQQLNESLS	FLGL
Dectin	Dectin VSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFLGL	SFGSSCYLIST	TKENFWSTSE(2NCVQMGAHI	JVVINTEAEON	FITQQLNESLS	FLGL
	80	06	100	110	120	130	140
	150	160			170		
mT405	mT405 SDPKVMANGNGSMILLSVKMSGSGTPMNP-	SMILLSVKMS	SSGTPMNP	1 1 1 1 1	E-	QKSGVFQ	VFQ
		::			•••	:	•
Dectin	Dectin SDPQGNGKWQWIDDTPFSQNVRFWHPHEPNLPEERCVSIVYWNPSKWGWNDVFCDSKHNSICEMKKIYL	FPESQNVRFWI	HEPNLPEE	SCVSIVYWNE	SKWGWNDVFC	DSKHNSICEMKE	TXL
	150	160	170	180	190	200	

Fig. 4I

OOPESST Offor

70 70 70	140 YFL	YFL 140	TAT :::
TCFS	SESY.	SLSY	CEMNK
60 LSELHSYHSSI : ::::::: LYELHTYHSSI 60	130 EQNFIVQQLNI	EQNFITQQLNI 130	SAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKINGOTER STATE
50 HFTYGETGKR. .:: QFIMDQPSRR. 50	120 AHLVVFNTEAD	AHLVVINTEA 120	190 WKPTGWGWND': :::::
20	90 130 110 120 130 14 WKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYF	TSEQNCVQMG,	160 170 180 190 200 DKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL ::.::::::::::::::::::::::::::::::::::
30 GISIALLSA :::::: VISMLLLST 30	100 ISSEEKVWS	ISTKENFWS 100	170 FWHLGEPNH : ::: FWHPHEPNI 170
20 WLSLRLWSVA : .:::::: W-TLRLWSAA	90 WKSFGSSCYF	WKSFGSSCYL 90	160 DKTPYEKNVRFWH :::::: DDTPFSQNVRFWH
10 20 30 40 50 60 70 hT405 MMQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG ::::::::::::::::::::::::::::::::::::	80 90 100 110 120 130 140 hT405 TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL	_	150 hT405 GLSDPQGNNNWQWII ::::: ::::: Dectin GLSDPQGNGKWQWII
hT405 Dectin	hT405	Dectin	hT405 Dectin

Fig. 4M

DOYKESII SIIISOI

60 120 178	226	274	322	370	418
ACT TGA A	೮ ವ	⊢	υo	υø	K 0 0
ITA) CCC' AAC,	CTG	TGT Cys	CCC	TGC Cys	CCA Pro 80
GCATTTAACT AGGTCCCTGA CCTCAACA	ACC Thr 15	ACC Thr	CAG Gln	ACC Thr	TGC Cys
_	TGG Trp	AGT Ser 30	GAC Asp	CTC Leu	TGC Cys
CCGCTCTGTG GACAGAAGCC TGAACATACA	TGC Cys	TTG Leu	ATG Met 45	AGT Ser	GGA Gly
CCGC GAC <i>I</i> TGA <i>I</i>	GTC Val	CTC Leu	ATT Ile	TCC Ser 60	TGG Trp
GGC	GGA Gly	TTA Leu	TTT Phe	CAT His	ATG Met 75
CAGCATTGGC TGGCCTCTTT CCTGACCTTC	AAG Lys 10	ATG Met	CAA Gln	TAC Tyr	AAA Lys
_	666 61y	TCC Ser 25	TAC Tyr	ACA Th <i>r</i>	GAA Glu
TCTGGGTTTG TTCTGAACTC GCAAGAAACC	CAA Gln	ATT Ile	ACT Thr 40	CAC His	TCA Ser
TGGG	TCC Ser	GTG Val	GTG Val	CTT Leu 55	GTG Val
	CAA Gln	GCT Ala	GTG Val	GAA Glu	ATG Met 70
TGACAGTTCACAGA	AGA Arg 5	GCT Ala	TGT Cys	TAT Tyr	ACT Thr
TCCGCTGACT TGGAAGTTGA GGAGACAGAT	GAA Glu	TCA Ser 20	AGC Ser	CTA Leu	GGG G1γ
	CAG Gln	TGG Trp	GCG Ala 35	AGA Arg	GAA Glu
CGACCCCGCG CAAGTGTGTG GTCGTATTTT	GTG Val	CTC	ATT Ile	AGA Arg 50	AGT Ser
CGAC CAAG GTCG	ATG Met 1	AGA Arg	TTC Phe	AGT Ser	TTC Phe 65

Fig. 4N

466	514	562	610	658	902
AAG Lys	GCT Ala	CAG Gln	CAA Gln	AAT Asn 160	TGT Cys
ACC Thr 95	666 61y	ACC Thr	CCA Pro	CAA	CGG Arg 175
TCT Ser	ATG Met 110	ATC Ile	GAT Asp	AGT Ser	GAG Glu
ATT Ile	CAG Gln	TTC Phe 125	TCG Ser	TTC Phe	GAA Glu
CTC Leu	GTT Val	AAT Asn	CTT Leu 140	CCT Pro	CCA Pro
TAC Tyr	TGT Cys	CAG Gln	GGT Gly	ACT Thr 155	CTT Leu
TGC Cys 90	AAC Asn	GAG Glu	CTG Leu	GAT Asp	AAT Asn 170
AGC Ser	CAG Gln 105	GCG Ala	TTC Phe	GAT Asp	CCC Pro
TCC Ser	GAG Glu	GAA Glu 120	TAC Tyr	ATC Ile	GAA Glu
GGC Gly	AGT Ser	ACT Thr	TCT Ser 135	TGG Trp	CAT His
TTT Phe	ACC Th <i>r</i>	AAT Asn	CTT	CAA Gln 150	CCC Pro
TCA Ser 85	AGC Ser	ATC Ile	TCA Ser	TGG Trp	CAC His 165
AAG Lys	TGG Trp 100	GTG Val	GAG Glu	AAA $L\gamma s$	TGG
rgg Irp	TTC Phe	GTG Val 115	AAT Asn	GGC Gly	TTC Phe
CAC '	AAC Asn	CTG Leu	CTG Leu 130	AAT Asn	AGG Arg
AAT Asn	GAG Glu	CAT His	CAG Gln	GGT Gly 145	GTC Val

Fig. 40

IDVEKKII DIIBII

754	802	858	918 978 1038 1098 1158 1218
	ω	ω	
TCG AAA TGG GGC TGG AAT GAT GTT Ser Lys Trp Gly Trp Asn Asp Val 185	AAA CAC AAT TCA ATA TGT GAA ATG AAG AAG ATT TAC Lys His Asn Ser Ile Cys Glu Met Lys Lys Ile Tyr 200	GTTA TTCATTAATA TCTTTAAAGT TCAGACCTAC CAAGAAGCCA	CCTAGCCACT ATTCTTTACT TTGTCAACTT GACACAAACT CTCTGTCAGC TTGACCAGTC AGAGGGTCCA GGTGGTAAGC TCCATCCATC TCTGCCCTCA ACTGCTTA CTTGAAAGTA
6.00	AT(AGA	•
TGG	GAA Glu	T TC	TTTT AGTT TTGC TGTA ATCA
AAA Lys	TGT Cys	AAAG	CCGTTCTTTT GGTTAGAGTT AAGGAATTGC GATTGTTGTA GGGAGCATCA CTTTCTATGA AAAA
TCG / Ser] 185	ATA Ile	TTT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	TCA Ser 200	'A TC	GAGG TGAT AGCT TAAT GCCA
AAT CCT Asn Pro	AAA CAC AAT Lys His Asn	ITAAI	CTGACAGAGG CCGT TCCTTCTGAT GGTT. ATCTTCAGCT AAGG. CTTGATTAAT GATT. GAGCAAGCCA GGGA GCCCTGGTTT CTTT.
TGG Trp	CAC His	TCAI	
TAC TGG Tyr Trp	AAA Lys	TA T	TACA CTTT GTAG ATTT ATGA GTCT
GTT Val 180		CTGT	TAACTTCTTG GCCTGTACAT CAAACAGAAT GAGCCCTTTC AGAGTCACCT GGGGAGTAGG AGCATGTCTG GGGCCATTTT AAAGGTGTTA AACCCATGAA GGTTTCTGCC CCAGGGTCTT TAAGATGAAT AAACAATTTC
	TTC TGT GAT AGT Phe Cys Asp Ser 195	CTA TGA GTGCCT(Leu *	A PER
TCA ATA Ser Ile	TGT Cys	TGA *	CAGA CAGA STCAC NTGTC SGTGT
GTT Val	TTC Phe	CTA Leu	TAAC CAAA AGAG AGCA AAAG GGTT

DOVERSAL OLIMOA

GTTC GTTC GCTA GGAA	CGAC TGAC GGCT	CCAC STTTG GCTC	GCG1 TAAT CTTG	GTCGACCCACGCGTCCGGAAACCATTCCACAATCACCCTCCTGAGGAACTCTTAGCACTGCATAAAGT GTTCTGAGTTTGTAATCAGATATTGTCACACTGGTTCCTTCAAACAGACATGACAAGGAGCTGGCTTTGG GCTAGGCTGCTCCTTGCCTATGATTGGGGAAGGTTAAACCCCTACAGGGCTTATGTATG	AAAC TATT TGAT	CATT GTCA TGGG	CCAC CACT GAAG	AATC GGTT GTTA	ACCC CCTI AACC	TCCT CAAP CCCTP	TGAGG ACAGA ACAGG	SAACT ACATG SGCTT	CTTF SACAF	AGCAC AGGAC PATGI	TGCP CTGC GGAP	CTGCATAAAGT GCTGGCTTTGG TGGAAACTGTT TTGAGTAAAAG	.GT .GG .TT .AG	68 138 208 278
AACT	GCTA	TCCA	CAAP	ACACC	ATTA	ATCC	TTTA	GGGA	GGC⊅	1GAA?	AAGGC	CAGP	M A ATG	O G CAA	S AGC	H CAT	M Q S H L AACTGCTATCCACAAACACCATTAATCCTTTAGGGAGGCAGAAAAGGCCAGA ATG CAA AGC CAT CTT	5 345
F	I ATT	F I T L G TTC ATT ACA CTA GGG	L CTA	G GGG	S TCT	V GTC	F TTT	L TTA	L	CHC	W TGG	A GCC	H H H H	I ATC	W TGG	G GGA	999	23 399
H CAT	V GTT	H V S P T CAT GTT TCC CCC ACT	CCC	TACT	W TGG	N AAC	S AGT	E GAG	P CCT	9 9	Q CAG	D GAC	S AGT	N AAC	L CTG	W TGG	T W N S E P G Q D S N L W A CT TGG AAC AGT GAG CCT GGC CAG GAC AGT AAC CTG TGG GCT 4	41 453
$_{\rm TGT}^{\rm C}$	D GAT	C D D I I TGT GAT GAC ATT ATT	I ATT	I ATT	S TCT	N AAT	R AGG	E GAA	W TGG	E GAA	R AGG	M ATG	$_{ m L}$	A GCT	S TCT	Q CAG	V GTT	59 507
$_{ m L}$	K AAG	L K C P G TTA AAG TGT CCT GGA	PCCT	GGA	G GGA	E GAA	E GAG	K AAA	G GGA	R CGA	H CAT	E GAG	K AAG	E GAG	T ACA	M ATG	K AAG	77
K AAG AGAT	M ATG	K M G E G AAG ATG GGT GAG GGG AGATACTGTGGGAGAACGA	E GAG SAGAP	K M G E G AAG ATG GGT GAG GGG A AGATACTGTGGGAGAACGAT.	E GAG	I ATA 'GCAG	V GTG SAGGG	TAAG	ACCC	TGAC	SAATC	GCATAGGA	'AGGC AGAAC	STAAP	ACTO	E I V GAG ATA GTG TAAGACCCTGAGAATGGCATAGGGTAAAACTGGGACAG AGCTGCAGAGGACAGGAGGAAGGAAGGAAGAAGAAGAAGAAGAA	AA	∞ N 0
ACAG	TTTC	GAGA AGATC	AAACI	ACAGTTTGGAGAAACTCTCACAATACATTCATAAGAAGACAAAGAACCCAATAAAAATGGGCAACAGATA CCACAGAAGATGATATATTGAGTGGCCAATAAATACATAAAAATTGCTCAACATCTATAATTACCAGGG	ACAAT	'ACAT	TCAT	AAGA	AGAC	AAAG AAAAT	SAACC	CAAT	'AAAA ACATO	AATGC	GCAP	CAATACATTCATAAGAAGACAAAGAACCCAATAAAAATGGGCAACAGATA AGTGGCCAATAAATACATAAAAATATGCTCAACATCTATAATTACCAGGG	TA	763 833
AAAT	GCAC	AATT? TTTC	AAAAC 3GGAG	AAATGCAAATTAAAAGCACTGTGAGATACCACTACACACTGATGAGAATGGCTAAAATCAAAAAAAGACCA ACCAGCACTTTGGGAGGCCGAGGTGGGCGGATCATGAGGTCAGGAGTTTGAGACTAGCCTGACCAACATG	GTGA	GATA GGGC	CCAC	TACA	CACT	GATC	SAGAA SAGTT	ATGGC TTGAG	TAAE	AATC? AGCCI	AAAA	GTGAGATACCACTACACCACTGATGAGAATGGCTAAAATCAAAAAAAGACCA AGGTGGGGGGATCATGAGGTCAGGAGTTTGAGACTAGCCTGACCAACATG	CA	903 973

Fig. 5A

GTGAAACCCTGTCTACTAAACATACAAAAATTAGCTGGGGGTGGTGGCATGCGCCTGTAATTCCAGCT	1043
ACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCAGAGATTACAGTGAGCCGAGATCATGC	1113
CCTTGCACTCTAGCCTGGGTGACAGAGCGAGACTCTGTCTTAAAAAAAA	1183
AAAAAAAAAGGGGGGCGC	1202

Fig. 5F

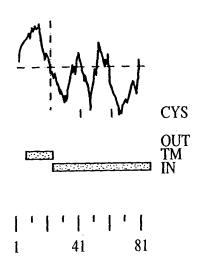


FIG. 5C